FIG. 1

PROTEIN ALIGNMENT OF MOUSE, HUMAN AND RAT Nav1.3

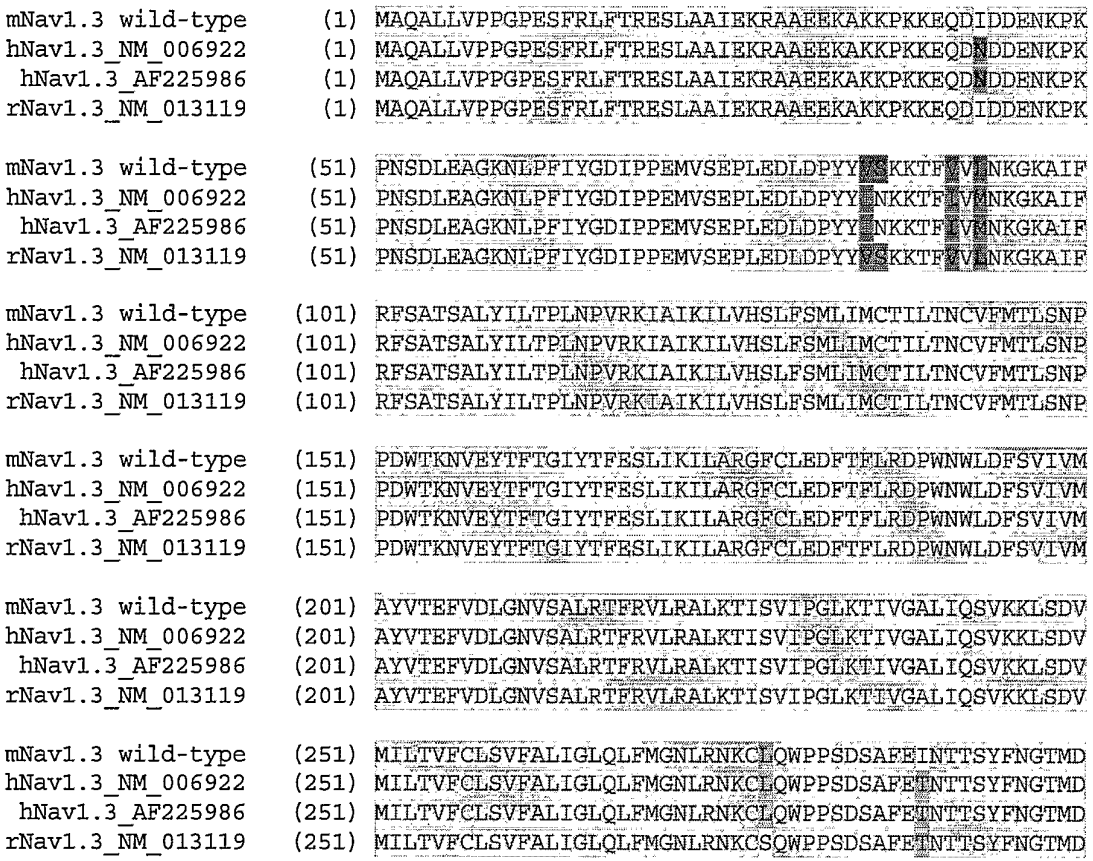

FIG. 1

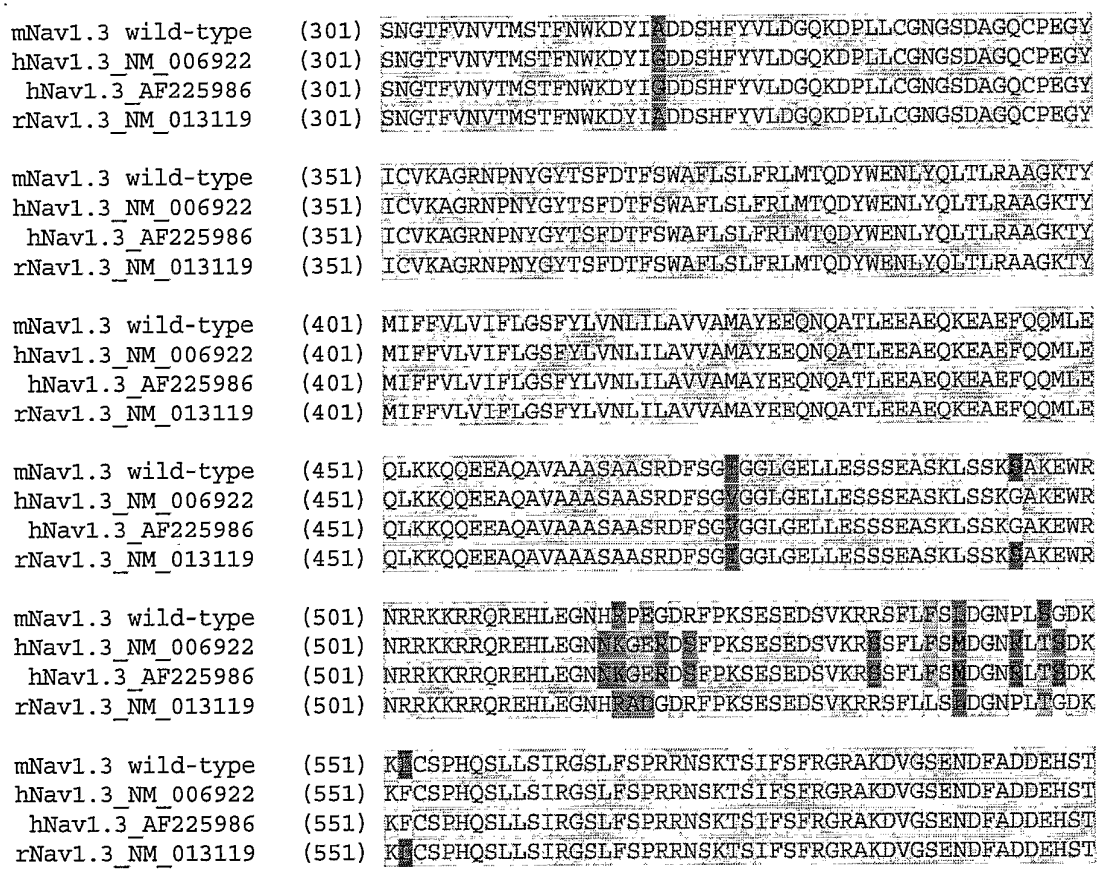
mNav1.3 wild-type (301) SNGTFVNVTMSTFNWKDYIADDSHFYVLDGQKDPLLCGNGSDAGQCPEGY
hNav1.3_NM_006922 (301) SNGTFVNVTMSTFNWKDYIGDDSHFYVLDGQKDPLLCGNGSDAGQCPEGY
hNav1.3_AF225986 (301) SNGTFVNVTMSTFNWKDYIGDDSHFYVLDGQKDPLLCGNGSDAGQCPEGY
rNav1.3_NM_013119 (301) SNGTFVNVTMSTFNWKDYIADDSHFYVLDGQKDPLLCGNGSDAGQCPEGY
mNav1.3 wild-type (351) ICVKAGRNPNYGYTSFDTFSWAFLSLFRLMTQDYWENLYQLTLRAAGKTY
hNav1.3_NM_006922 (351) ICVKAGRNPNYGYTSFDTFSWAFLSLFRLMTQDYWENLYQLTLRAAGKTY
hNav1.3_AF225986 (351) ICVKAGRNPNYGYTSFDTFSWAFLSLFRLMTQDYWENLYQLTLRAAGKTY
rNav1.3_NM_013119 (351) ICVKAGRNPNYGYTSFDTFSWAFLSLFRLMTQDYWENLYQLTLRAAGKTY
mNav1.3 wild-type (401) MIFFVLVIFLGSFYLVNLILAVVAMAYEEQNQATLEEAEQKEAEFQQMLE
hNav1.3_NM_006922 (401) MIFFVLVIFLGSFYLVNLILAVVAMAYEEQNQATLEEAEQKEAEFQQMLE
hNav1.3_AF225986 (401) MIFFVLVIFLGSFYLVNLILAVVAMAYEEQNQATLEEAEQKEAEFQQMLE
rNav1.3_NM_013119 (401) MIFFVLVIFLGSFYLVNLILAVVAMAYEEQNQATLEEAEQKEAEFQQMLE
mNav1.3 wild-type (451) QLKKQQEEAQAVAAASAASRDFSGAGGLGELLESSSEASKLSSKSAKEWR
hNav1.3_NM_006922 (451) QLKKQQEEAQAVAAASAASRDFSGVGGLGELLESSSEASKLSSKGAKEWR
hNav1.3_AF225986 (451) QLKKQQEEAQAVAAASAASRDFSGVGGLGELLESSSEASKLSSKGAKEWR
rNav1.3_NM_013119 (451) QLKKQQEEAQAVAAASAASRDFSGAGGLGELLESSSEASKLSSKSAKEWR
mNav1.3 wild-type (501) NRRKKRRQREHLEGNHRPEGDRFPKSESEDSVKRRSFLFSRDGNPLSGDK
hNav1.3_NM_006922 (501) NRRKKRRQREHLEGNNKGERDSFPKSESEDSVKRRSFLFSMDGNRLTSDK
hNav1.3_AF225986 (501) NRRKKRRQREHLEGNNKGERDSFPKSESEDSVKRRSFLFSMDGNRLTSDK
rNav1.3_NM_013119 (501) NRRKKRRQREHLEGNHRAIGDRFPKSESEDSVKRRSFLLSRDGNPLTGDK
mNav1.3 wild-type (551) KTCSPHQSLLSIRGSLFSPRRNSKTSIFSFRGRAKDVGSENDFADDEHST
hNav1.3_NM_006922 (551) KFCSPHQSLLSIRGSLFSPRRNSKTSIFSFRGRAKDVGSENDFADDEHST
hNav1.3_AF225986 (551) KFCSPHQSLLSIRGSLFSPRRNSKTSIFSFRGRAKDVGSENDFADDEHST
rNav1.3_NM_013119 (551) KTCSPHQSLLSIRGSLFSPRRNSKTSIFSFRGRAKDVGSENDFADDEHST

FIG. 1

```
mNav1.3 wild-type    (601) FEDSESRRDSLFVPHRPGERRNSNVSQASMSSRMVPGLPANGKMHSTVDC
hNav1.3_NM_006922    (601) FEDGESRRDSLFVPHRHGERRNSNVSQASMSSRMVPGLPANGKMHSTVDC
 hNav1.3_AF225986    (601) FEDSESRRDSLFVPHRHGERRNSN--------------------------
rNav1.3_NM_013119    (601) FEDSESRRDSLFVPHRPGERRNSN--------------------------

mNav1.3 wild-type    (651) NGVVSL-----------------GTTTETEVRKRRLSSYQISMEMLEDSS
hNav1.3_NM_006922    (651) NGVVSLVGGPSALTSPTGQLPPEGTTTETEVRKRRLSSYQISMEMLEDSS
 hNav1.3_AF225986    (625) ----------------------GTTTETEVRKRRLSSYQISMEMLEDSS
rNav1.3_NM_013119    (625) ----------------------GTTTETEVRKRRLSSYQISMEMLEDSS

mNav1.3 wild-type    (684) GRQRAMSIASILTNTMEELEESRQKCPPCWYRFANVFLIWDCCDAWLKVK
hNav1.3_NM_006922    (701) GRQRAVSIASILTNTMEELEESRQKCPPCWYRFANVFLIWDCCDAWLKVK
 hNav1.3_AF225986    (652) GRQRAVSIASILTNTMEELEESRQKCPPCWYRFANVFLIWDCCDAWLKVK
rNav1.3_NM_013119    (652) GRQRSMSIASILTNTMEELEESRQKCPPCWYRFANVFLIWDCCDAWLKVK

mNav1.3 wild-type    (734) HLVNLIVMDPFVDLAITICIVLNTLFMAMEHYPMTEQFSSVLTVGNLVFT
hNav1.3_NM_006922    (751) HLVNLIVMDPFVDLAITICIVLNTLFMAMEHYPMTEQFSSVLTVGNLVFT
 hNav1.3_AF225986    (702) HLVNLIVMDPFVDLAITICIVLNTLFMAMEHYPMTEQFSSVLTVGNLVFT
rNav1.3_NM_013119    (702) HLVNLIVMDPFVDLAITICIVLNTLFMAMEHYPMTQQFSSVLTVGNLVFT

mNav1.3 wild-type    (784) GIFTAEMVLKIIAMDPYYYFQEGWNIFDGIIVSLSLMELGLANVEGLSVL
hNav1.3_NM_006922    (801) GIFTAEMVLKIIAMDPYYYFQEGWNIFDGIIVSLSLMELGLSNVEGLSVL
 hNav1.3_AF225986    (752) GIFTAEMVLKIIAMDPYYYFQEGWNIFDGIIVSLSLMELGLSNVEGLSVL
rNav1.3_NM_013119    (752) GIFTAEMVLKIIAMDPYYYFQEGWNIFDGIIVSLSLMELGLANVEGLSVL

mNav1.3 wild-type    (834) RSFRLLRVFKLAKSWPTLNMLIKIIGNSVGALGNLTLVLAIIVFIFAVVG
hNav1.3_NM_006922    (851) RSFRLLRVFKLAKSWPTLNMLIKIIGNSVGALGNLTLVLAIIVFIFAVVG
 hNav1.3_AF225986    (802) RSFRLLRVFKLAKSWPTLNMLIKIIGNSVGALGNLTLVLAIIVFIFAVVG
rNav1.3_NM_013119    (802) RSFRLLRVFKLAKSWPTLNMLIKIIGNSVGALGNLTLVLAIIVFIFAVVG

mNav1.3 wild-type    (884) MQLFGKSYKECVCKINDDCKLPRWHMNDFFHSFLIVFRVLCGEWIETMWD
```

FIG. 1

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hNav1.3_NM_006922    (901) MQLFGKSYKECVCKINDDCTLPRWHMNDFFHSFLIVFRVLCGEWIETMWD
 hNav1.3_AF225986    (852) MQLFGKSYKECVCKINDDCTLPRWHMNDFFHSFLIVFRVLCGEWIETMWD
rNav1.3_NM_013119    (852) MQLFGKSYKECVCKINVDCKLPRWHMNDFFHSFLIVFRVLCGEWIETMWD

mNav1.3 wild-type    (934) CMEVAGQTMCLIVFMLVMVIGNLVVLNLFLALLLSSFSSDNLAATDDDNE
hNav1.3_NM_006922    (951) CMEVAGQTMCLIVFMLVMVIGNLVVLNLFLALLLSSFSSDNLAATDDDNE
 hNav1.3_AF225986    (902) CMEVAGQTMCLIVFMLVMVIGNLVVLNLFLALLLSSFSSDNLAATDDDNE
rNav1.3_NM_013119    (902) CMEVAGQTMCLIVFMLVMVIGNLVVLNLFLALLLSSFSSDNLAATDDDNE

mNav1.3 wild-type    (984) MNNLQIAVGRMQKGIDYVKNKMRECFQKAFFRKPKVIEIHEGNKIDSCMS
hNav1.3_NM_006922   (1001) MNNLQIAVGRMQKGIDYVKNKMRECFQKAFFRKPKVIEIHEGNKIDSCMS
 hNav1.3_AF225986    (952) MNNLQIAVGRMQKGIDYVKNKMRECFQKAFFRKPKVIEIHEGNKIDSCMS
rNav1.3_NM_013119    (952) MNNLQIAVGRMQKGIDFVKNKMRECFQKAFFRKPKVIEIQEGNKIDSCMS

mNav1.3 wild-type   (1034) NNTGSIEISKELNYLKDGNGTTSGVGTGSSVEKYVIDENDYMSFINNPSL
hNav1.3_NM_006922   (1051) NNTGI-EISKELNYLKDGNGTTSGVGTGSSVEKYVIDENDYMSFINNPSL
 hNav1.3_AF225986   (1002) NNTGI-EISKELNYLKDGNGTTSGVGTGSSVEKYVIDENDYMSFINNPSL
rNav1.3_NM_013119   (1002) NNTGI-EISKELNYLKDGNGTTSGVGTGSSVEKYVIDENDYMSFINNPSL

mNav1.3 wild-type   (1084) TVTVPIAVGESDFENLNTEEFSSESELEESKEKLNATSSSEGSTVDVALP
hNav1.3_NM_006922   (1100) TVTVPIAVGESDFENLNTEEFSSESELEESKEKLNATSSSEGSTVDVVLP
 hNav1.3_AF225986   (1051) TVTVPIAVGESDFENLNTEEFSSESELEESKEKLNATSSSEGSTVDVVLP
rNav1.3_NM_013119   (1051) TVTVPIAVGESDFENLNTEEFSSESELEESKEKLNATSSSEGSTVDVALP

mNav1.3 wild-type   (1134) REGEQAEIEPEEDLKPEACFTEGCIKKFPFCQVSTEEGKGKIWWNLRKTC
hNav1.3_NM_006922   (1150) REGEQAEIEPEEDFKPEACFTEGCIKKFPFCQVSTEEGKGKIWWNLRKTC
 hNav1.3_AF225986   (1101) REGEQAEIEPEEDFKPEACFTEGCIKKFPFCQVSTEEGKGKIWWNLRKTC
rNav1.3_NM_013119   (1101) REGEQAEIEPEEDLKPEACFTEGCIKKFPFCQVSTEEGKGKIWWNLRKTC

mNav1.3 wild-type   (1184) YSIVEHNWFETFIVFMILLSSGALAFEDIYIEQRKTIKTMLEYADKVFTY
hNav1.3_NM_006922   (1200) YSIVEHNWFETFIVFMILLSSGALAFEDIYIEQRKTIKTMLEYADKVFTY
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FIG. 1

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 hNav1.3_AF225986  (1151) YSIVEHNWFETFIVFMILLSSGALAFEDIYIEQRKTIKTMLEYADKVFTY
rNav1.3_NM_013119  (1151) YSIVEHNWFETFIVFMILLSSGALAFEDIYIEQRKTIKTMLEYADKVFTY

mNav1.3 wild-type  (1234) IFILEMLLKWVAYGFQTYFTNAWCWLDFLIVDVSLVSLVANALGYSELGA
hNav1.3_NM_006922  (1250) IFILEMLLKWVAYGFQTYFTNAWCWLDFLIVDVSLVSLVANALGYSELGA
 hNav1.3_AF225986  (1201) IFILEMLLKWVAYGFQTYFTNAWCWLDFLIVDVSLVSLVANALGYSELGA
rNav1.3_NM_013119  (1201) IFILEMLLKWVAYGFQTYFTNAWCWLDFLIVDVSLVSLVANALGYSELGA

mNav1.3 wild-type  (1284) IKSLRTLRALRPLRALSRFEGMRVVVNALVGAIPSIMNVLLVCLIFWLIF
hNav1.3_NM_006922  (1300) IKSLRTLRALRPLRALSRFEGMRVVVNALVGAIPSIMNVLLVCLIFWLIF
 hNav1.3_AF225986  (1251) IKSLRTLRALRPLRALSRFEGMRVVVNALVGAIPSTMNVLLVCLIFWLIF
rNav1.3_NM_013119  (1251) IKSLRTLRALRPLRALSRFEGMRVVVNALVGAIPSIMNVLLVCLIFWLIF

mNav1.3 wild-type  (1334) SIMGVNLFAGKFYHCVNMTTGSMFDMSDVNNFSDCQALGKQARWKNVKVN
hNav1.3_NM_006922  (1350) SIMGVNLFAGKFYHCVNMTTGNMFDISDVNNFSDCQALGKQARWKNVKVN
 hNav1.3_AF225986  (1301) SIMGVNLFAGKFYHCVNTTTGNMFEIKDVNNFSDCQALGKQARWKNVKVN
rNav1.3_NM_013119  (1301) SIMGVNLFAGKFYHCVNTTTGNMFEIKDVNNFSDCQALGKQARWKNVKVN

mNav1.3 wild-type  (1384) FDNVGAGYLALLQVATFKGWMDIMYAAVDSRDVKLQPVYEENLYMYLYFV
hNav1.3_NM_006922  (1400) FDNVGAGYLALLQVATFKGWMDIMYAAVDSRDVKLQPVYEENLYMYLYFV
 hNav1.3_AF225986  (1351) FDNVGAGYLALLQVATFKGWMDIMYAAVDSRDVKLQPVYEENLYMYLYFV
rNav1.3_NM_013119  (1351) FDNVGAGYLALLQVATFKGWMDIMYAAVDSRDVKLQPIYEENLYMYLYFV

mNav1.3 wild-type  (1434) IFIIFGSFFTLNLFIGVIIDNFNQQKKKFGGQDIFMTEEQKKYYNAMKKL
hNav1.3_NM_006922  (1450) IFIIFGSFFTLNLFIGVIIDNFNQQKKKFGGQDIFMTEEQKKYYNAMKKL
 hNav1.3_AF225986  (1401) IFIIFGSFFTLNLFIGVIIDNFNQQKKKFGGQDIFMTEEQKKYYNAMKKL
rNav1.3_NM_013119  (1401) IFIIFGSFFTLNLFIGVIIDNFNQQKKKFGGQDIFMTEEQKKYYNAMKKL

mNav1.3 wild-type  (1484) GSKKPQKPIPRPANKFQGMVFDFVTRQVFDISIMILICLNMVTMMVETDD
hNav1.3_NM_006922  (1500) GSKKPQKPIPRPANKFQGMVFDFVTRQVFDISIMILICLNMVTMMVETDD
 hNav1.3_AF225986  (1451) GSKKPQKPIPRPANKFQGMVFDFVTRQVFDISIMILICLNMVTMMVETDD
```

FIG. 1

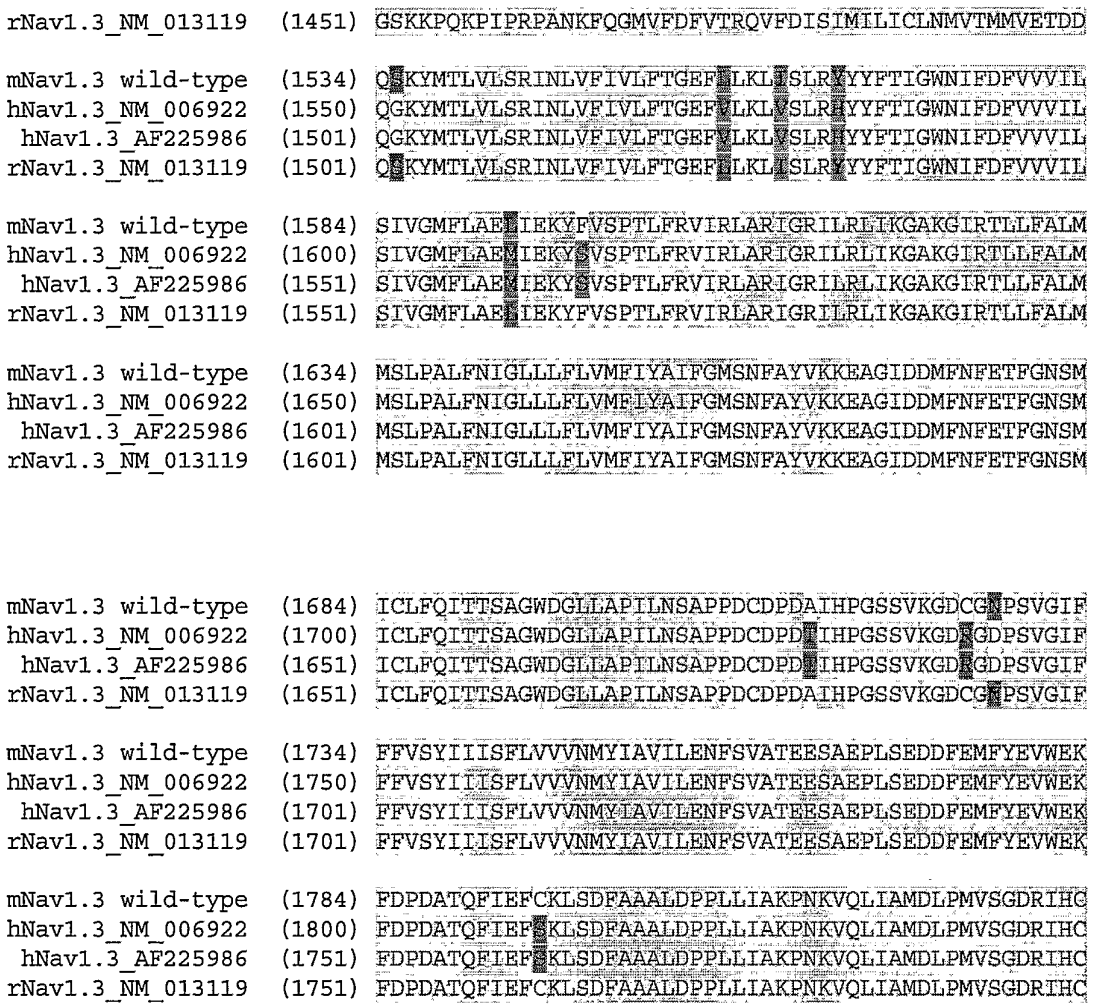
rNav1.3_NM_013119 (1451) GSKKPQKPIPRPANKFQGMVFDFVTRQVFDISIMILICLNMVTMMVETDD
mNav1.3 wild-type (1534) QSKYMTLVLSRINLVFIVLFTGEFMLKLISLRYYYFTIGWNIFDFVVVIL
hNav1.3_NM_006922 (1550) QGKYMTLVLSRINLVFIVLFTGEFVLKLVSLRHYYFTIGWNIFDFVVVIL
hNav1.3_AF225986 (1501) QGKYMTLVLSRINLVFIVLFTGEFVLKLVSLRHYYFTIGWNIFDFVVVIL
rNav1.3_NM_013119 (1501) QSKYMTLVLSRINLVFIVLFTGEFMLKLISLRYYYFTIGWNIFDFVVVIL
mNav1.3 wild-type (1584) SIVGMFLAEIIEKYFVSPTLFRVIRLARIGRILRLIKGAKGIRTLLFALM
hNav1.3_NM_006922 (1600) SIVGMFLAEMIEKYSVSPTLFRVIRLARIGRILRLIKGAKGIRTLLFALM
hNav1.3_AF225986 (1551) SIVGMFLAEMIEKYSVSPTLFRVIRLARIGRILRLIKGAKGIRTLLFALM
rNav1.3_NM_013119 (1551) SIVGMFLAEIIEKYFVSPTLFRVIRLARIGRILRLIKGAKGIRTLLFALM
mNav1.3 wild-type (1634) MSLPALFNIGLLLFLVMFIYAIFGMSNFAYVKKEAGIDDMFNFETFGNSM
hNav1.3_NM_006922 (1650) MSLPALFNIGLLLFLVMFIYAIFGMSNFAYVKKEAGIDDMFNFETFGNSM
hNav1.3_AF225986 (1601) MSLPALFNIGLLLFLVMFIYAIFGMSNFAYVKKEAGIDDMFNFETFGNSM
rNav1.3_NM_013119 (1601) MSLPALFNIGLLLFLVMFIYAIFGMSNFAYVKKEAGIDDMFNFETFGNSM
mNav1.3 wild-type (1684) ICLFQITTSAGWDGLLAPILNSAPPDCDPDAIHPGSSVKGDCGNPSVGIF
hNav1.3_NM_006922 (1700) ICLFQITTSAGWDGLLAPILNSAPPDCDPDTIHPGSSVKGDKGDPSVGIF
hNav1.3_AF225986 (1651) ICLFQITTSAGWDGLLAPILNSAPPDCDPDTIHPGSSVKGDKGDPSVGIF
rNav1.3_NM_013119 (1651) ICLFQITTSAGWDGLLAPILNSAPPDCDPDAIHPGSSVKGDCGNPSVGIF
mNav1.3 wild-type (1734) FFVSYIIISFLVVVNMYIAVILENFSVATEESAEPLSEDDFEMFYEVWEK
hNav1.3_NM_006922 (1750) FFVSYIIISFLVVVNMYIAVILENFSVATEESAEPLSEDDFEMFYEVWEK
hNav1.3_AF225986 (1701) FFVSYIIISFLVVVNMYIAVILENFSVATEESAEPLSEDDFEMFYEVWEK
rNav1.3_NM_013119 (1701) FFVSYIIISFLVVVNMYIAVILENFSVATEESAEPLSEDDFEMFYEVWEK
mNav1.3 wild-type (1784) FDPDATQFIEFCKLSDFAAALDPPLLIAKPNKVQLIAMDLPMVSGDRIHC
hNav1.3_NM_006922 (1800) FDPDATQFIEFSKLSDFAAALDPPLLIAKPNKVQLIAMDLPMVSGDRIHC
hNav1.3_AF225986 (1751) FDPDATQFIEFSKLSDFAAALDPPLLIAKPNKVQLIAMDLPMVSGDRIHC
rNav1.3_NM_013119 (1751) FDPDATQFIEFCKLSDFAAALDPPLLIAKPNKVQLIAMDLPMVSGDRIHC

FIG. 1

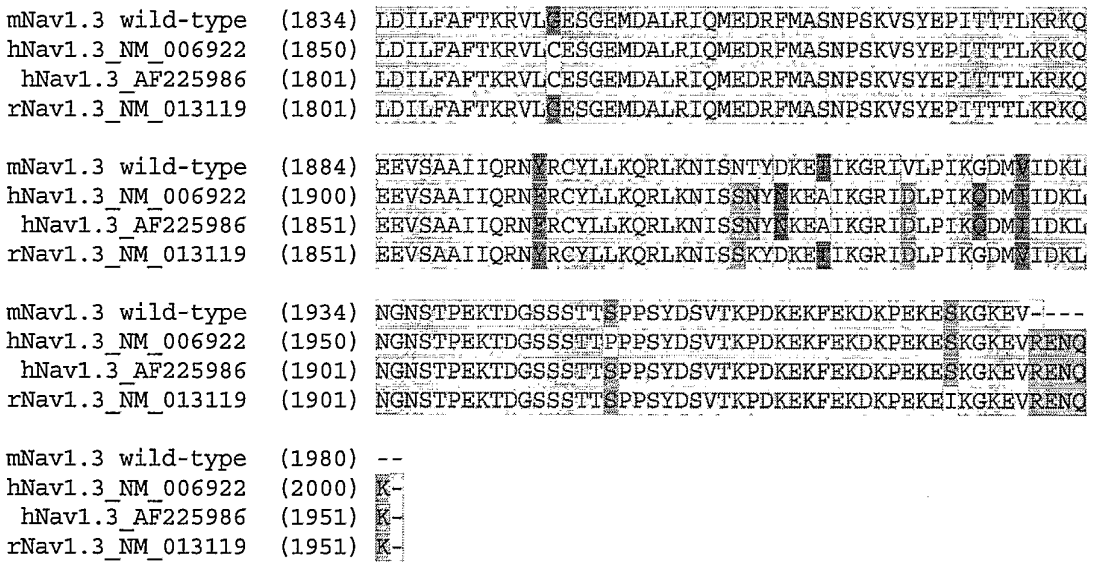
mNav1.3 wild-type (1834) LDILFAFTKRVLCESGEMDALRIQMEDRFMASNPSKVSYEPITTTLKRKQ
hNav1.3_NM_006922 (1850) LDILFAFTKRVLCESGEMDALRIQMEDRFMASNPSKVSYEPITTTLKRKQ
hNav1.3_AF225986 (1801) LDILFAFTKRVLCESGEMDALRIQMEDRFMASNPSKVSYEPITTTLKRKQ
rNav1.3_NM_013119 (1801) LDILFAFTKRVLCESGEMDALRIQMEDRFMASNPSKVSYEPITTTLKRKQ
mNav1.3 wild-type (1884) EEVSAAIIQRNYRCYLLKQRLKNISNTYDKETIKGRIVLPIKGDMYIDKL
hNav1.3_NM_006922 (1900) EEVSAAIIQRNFRCYLLKQRLKNISSNYNKEAIKGRIDLPIKQDMIIDKL
hNav1.3_AF225986 (1851) EEVSAAIIQRNFRCYLLKQRLKNISSNYNKEAIKGRIDLPIKQDMIIDKL
rNav1.3_NM_013119 (1851) EEVSAAIIQRNYRCYLLKQRLKNISSKYDKETIKGRIDLPIKGDMYIDKL
mNav1.3 wild-type (1934) NGNSTPEKTDGSSSTTSPPSYDSVTKPDKEKFEKDKPEKESKGKEV----
hNav1.3_NM_006922 (1950) NGNSTPEKTDGSSSTTPPPSYDSVTKPDKEKFEKDKPEKESKGKEVRENQ
hNav1.3_AF225986 (1901) NGNSTPEKTDGSSSTTSPPSYDSVTKPDKEKFEKDKPEKESKGKEVRENQ
rNav1.3_NM_013119 (1901) NGNSTPEKTDGSSSTTSPPSYDSVTKPDKEKFEKDKPEKEIKGKEVRENQ
mNav1.3 wild-type (1980) --
hNav1.3_NM_006922 (2000) K-
hNav1.3_AF225986 (1951) K-
rNav1.3_NM_013119 (1951) K-

FIG. 2

ALIGNMENT OF FULL-LENGTH AND PARTIAL MOUSE Nav1.3 PROTEIN

```
mNav1.3 wild-type     (1) MAQALLVPPGPESFRLFTRESLAAIEKRAAEEKAKKPKKE
mNav1.3 NM_018732         ----------------------------------------

mNav1.3 wild-type    (41) QDIDDENKPKPNSDLEAGKNLPFIYGDIPPEMVSEPLEDL
mNav1.3 NM_018732         ----------------------------------------

mNav1.3 wild-type    (81) DPYYVSKKTFVVLNKGKAIFRFSATSALYILTPLNPVRKI
mNav1.3 NM_018732         ----------------------------------------

mNav1.3 wild-type   (121) AIKILVHSLFSMLIMCTILTNCVFMTLSNPPDWTKNVEYT
mNav1.3 NM_018732         ----------------------------------------

mNav1.3 wild-type   (161) FTGIYTFESLIKILARGFCLEDFTFLRDPWNWLDFSVIVM
mNav1.3 NM_018732         ----------------------------------------

mNav1.3 wild-type   (201) AYVTEFVDLGNVSALRTFRVLRALKTISVIPGLKTIVGAL
mNav1.3 NM_018732         ----------------------------------------

mNav1.3 wild-type   (241) IQSVKKLSDVMILTVFCLSVFALIGLQLFMGNLRNKCLQW
mNav1.3 NM_018732         ----------------------------------------

mNav1.3 wild-type   (281) PPSDSAFEINTTSYFNGTMDSNGTFVNVTMSTFNWKDYIA
mNav1.3 NM_018732         ----------------------------------------

mNav1.3 wild-type   (321) DDSHFYVLDGQKDPLLCGNGSDAGQCPEGYICVKAGRNPN
mNav1.3 NM_018732         ----------------------------------------

mNav1.3 wild-type   (361) YGYTSFDTFSWAFLSLFRLMTQDYWENLYQLTLRAAGKTY
mNav1.3 NM_018732         ----------------------------------------
```

FIG. 2

```
mNav1.3 wild-type   (401) MIFFVLVIFLGSFYLVNLILAVVAMAYEEQNQATLEEAEQ
mNav1.3 NM_018732         ----------------------------------------

mNav1.3 wild-type   (441) KEAEFQQMLEQLKKQQEEAQAVAAASAASRDFSGIGGLGE
mNav1.3 NM_018732         ----------------------------------------

mNav1.3 wild-type   (481) LLESSSEASKLSSKSAKEWRNRRKKRRQREHLEGNHRPEG
mNav1.3 NM_018732         ----------------------------------------

mNav1.3 wild-type   (521) DRFPKSESEDSVKRRSFLFSLDGNPLSGDKKLCSPHQSLL
mNav1.3 NM_018732         ----------------------------------------

mNav1.3 wild-type   (561) SIRGSLFSPRRNSKTSIFSFRGRAKDVGSENDFADDEHST
mNav1.3 NM_018732         ----------------------------------------

mNav1.3 wild-type   (601) FEDSESRRDSLFVPHRPGERRNSNVSQASMSSRMVPGLPA
mNav1.3 NM_018732         ----------------------------------------

mNav1.3 wild-type   (641) NGKMHSTVDCNGVVSLGTTTETEVRKRRLSSYQISMEMLE
mNav1.3 NM_018732         ----------------------------------------

mNav1.3 wild-type   (681) DSSGRQRAMSIASILTNTMEELEESRQKCPPCWYRFANVF
mNav1.3 NM_018732         ----------------------------------------

mNav1.3 wild-type   (721) LIWDCCDSWLKVKHLVNLIVMDPFVDLAITICIVLNTLFM
mNav1.3 NM_018732         ----------------------------------------

mNav1.3 wild-type   (761) AMEHYPMTEQFSSVLTVGNLVFTGIFTAEMVLKIIAMDPY
mNav1.3 NM_018732         ----------------------------------------

mNav1.3 wild-type   (801) YYFQEGWNIFDGIIVSLSLMELGLANVEGLSVLRSFRLLR
mNav1.3 NM_018732         ----------------------------------------
```

FIG. 2

```
mNav1.3 wild-type   (841) VFKLAKSWPTLNMLIKIIGNSVGALGNLTLVLAIIVFIFA
mNav1.3 NM_018732     (1) -----------MLIKIIGNSVGALGNLTLVLAIIVFIFA

mNav1.3 wild-type   (881) VVGMQLFGKSYKECVCKINEDCKLPRWHMNDFFHSFLIVF
mNav1.3 NM_018732    (29) VVGMQLFGKSYKECVCKINEDCKLPRWHMNDFFHSFLIVF

mNav1.3 wild-type   (921) RVLCGEWIETMWDCMEVAGQTMCLIVFMLVMVIGNLVVLN
mNav1.3 NM_018732    (69) RVLCGEWIETMWDCMEVAGQTMCLIVFMLVMVIGNLVVLN

mNav1.3 wild-type   (961) LFLALLLSSFSSDNLAATDDDNEMNNLQIAVGRMQKGIDY
mNav1.3 NM_018732   (109) LFLALLLSSFSSDNLAATDDDNEMNNLQIAVGRMQKGIDY

mNav1.3 wild-type  (1001) VKNKIRECFRKAFFRKPKVIEIHEGNKIDSCMSNNTGVVE
mNav1.3 NM_018732   (149) VKNKIRECFRKAFFRKPKVIEIHEGNKIDSCMSNNTGVVE

mNav1.3 wild-type  (1041) ISKELNYLKDGNGTTSGVGTGSSVEKYVIDENDYMSFINN
mNav1.3 NM_018732   (189) ISKELNYLKDGNGTTSGVGTGSSVEKYVIDENDYMSFINN

mNav1.3 wild-type  (1081) PSLTVTVPIAVGESDFENLNTEEFSSESELEESKEKLNAT
mNav1.3 NM_018732   (229) PSLTVTVPIAVGESDFENLNTEEFSSESELEESKEVSALF

mNav1.3 wild-type  (1121) SSSEGSTVDVAPPREGEQAEPEPEEDLKPEACFTEGCIKK
mNav1.3 NM_018732   (269) SSGHHFCAIYTVWLLCIVFC----------------------

mNav1.3 wild-type  (1161) FPFCQVSTEEGKGKIWWNLRKTCYSIVEHNWFETFIVFMI
mNav1.3 NM_018732         ----------------------------------------

mNav1.3 wild-type  (1201) LLSSGALAFEDIYIEQRKTIKTMLEYADKVFTYIFILEML
mNav1.3 NM_018732         ----------------------------------------

mNav1.3 wild-type  (1241) LKWVAYGFQTYFTNAWCWLDFLIVDVSLVSLVANALGYSE
mNav1.3 NM_018732         ----------------------------------------

mNav1.3 wild-type  (1281) LGAIKSLRTLRALRPLRALSRFEGMRVVVNALVGAIPSIM
```

FIG. 2

```
mNav1.3 NM_018732          ----------------------------------------

mNav1.3 wild-type  (1321) NVLLVCLIFWLIFSIMGVNLFAGKFYHCVNMTTGSMFDMS
mNav1.3 NM_018732          ----------------------------------------

mNav1.3 wild-type  (1361) EVNNFSDCQALGKQARWKNVKVNFDNVGAGYLALLQVATF
mNav1.3 NM_018732          ----------------------------------------

mNav1.3 wild-type  (1401) KGWMDIMYAAVDSRDVKLQPVYEENLYMYLYFVIFIIFGS
mNav1.3 NM_018732          ----------------------------------------

mNav1.3 wild-type  (1441) FFTLNLFIGVIIDNFNQQKKKFGGQDIFMTEEQKKYYNAM
mNav1.3 NM_018732          ----------------------------------------

mNav1.3 wild-type  (1481) KKLGSKKPQKPIPRPANKFQGMVFDFVTRQVFDISIMILI
mNav1.3 NM_018732          ----------------------------------------

mNav1.3 wild-type  (1521) CLNMVTMMVETDDQSKYMTLVLSRINLVFIVLFTGEFLLK
mNav1.3 NM_018732          ----------------------------------------

mNav1.3 wild-type  (1561) LISLRYYYFTIGWNIFDFVVVILSIVGMFLAELIEKYFVS
mNav1.3 NM_018732          ----------------------------------------

mNav1.3 wild-type  (1601) PTLFRVIRLARIGRILRLIKGAKGIRTLLFALMMSLPALF
mNav1.3 NM_018732          ----------------------------------------

mNav1.3 wild-type  (1641) NIGLLLFLVMFIYAIFGMSNFAYVKKEAGIDDMFNFETFG
mNav1.3 NM_018732          ----------------------------------------

mNav1.3 wild-type  (1681) NSMICLFQITTSAGWDGLLAPILNSAPPDCDPDAIHPGSS
mNav1.3 NM_018732          ----------------------------------------

mNav1.3 wild-type  (1721) VKGDCGNPSVGIFFFVSYIIISFLVVVNMYIAVILENFSV
mNav1.3 NM_018732          ----------------------------------------
```

FIG. 2

```
mNav1.3 wild-type  (1761) ATEESAEPLSEDDFEMFYEVWEKFDPDATQFIEFCKLSDF
mNav1.3 NM_018732         ----------------------------------------

mNav1.3 wild-type  (1801) AAALDPPLLIAKPNKVQLIAMDLPMVSGDRIHCLDILFAF
mNav1.3 NM_018732         ----------------------------------------

mNav1.3 wild-type  (1841) TKRVLGESGEMDALRIQMEDRFMASNPSKVSYEPITTTLK
mNav1.3 NM_018732         ----------------------------------------

mNav1.3 wild-type  (1881) RKQEEVSAAIIQRNYRCYLLKQRLKNISNTYDKETIKGRI
mNav1.3 NM_018732         ----------------------------------------

mNav1.3 wild-type  (1921) VLPIKGDMVIDKLNGNSTPEKTDGSSSTTSPPSYDSVTKP
mNav1.3 NM_018732         ----------------------------------------

mNav1.3 wild-type  (1961) DKEKFEKDKPEKESKGKEV
mNav1.3 NM_018732         --------------------
```

FIG. 3

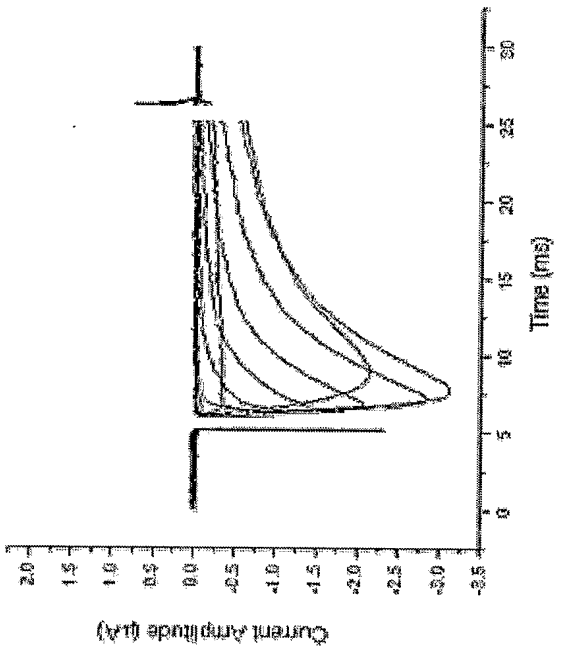
Current Amplitude (μA)
2.0
1.5
1.0
0.5
0.0
-0.5
-1.0
-1.5
-2.0
-2.5
-3.0
-3.5
0
5
10
15
20
25
30
Time (ms)

FIG. 4

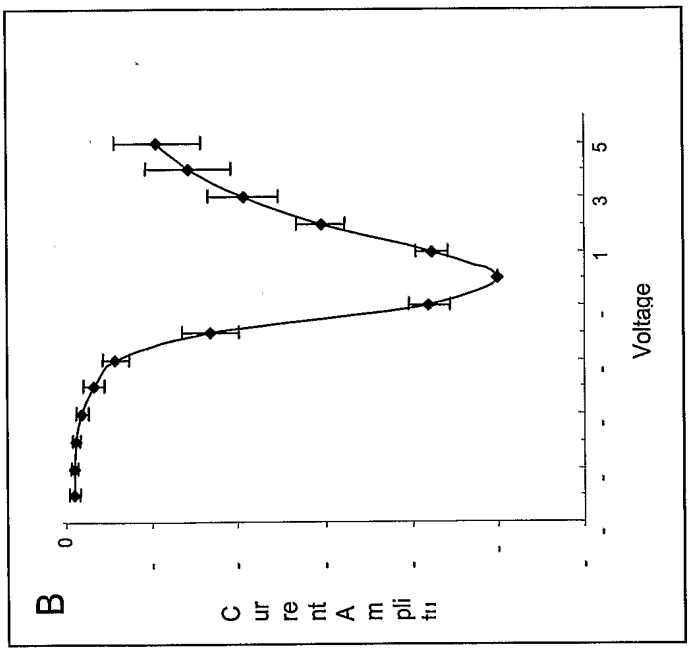

FIG. 5

SEQ ID NO:1

ATGGCCCAGGCACTGCTGGTACCCCCGGGACCTGAGAGCTTCC
GCCTTTTCACTCGAGAATCTCTTGCTGCTATCGAAAAGCGTGCTGCAGAA
GAGAAAGCCAAGAAACCCAAGAAAGAACAAGACATTGACGATGAGAACAA
GCCAAAGCCAAACAGTGACTTGGAAGCTGGGAAGAACCTTCCATTTATCT
ATGGAGACATTCCTCCAGAGATGGTGTCGGAGCCTCTGGAGGACCTGGAC
CCCTACTACGTCAGTAAGAAAACTTTTGTAGTGTTGAATAAAGGGAAGGC
AATTTTTCGATTCAGTGCCACCTCCGCCTTGTATATTTTAACTCCACTAA
ACCCCGTTAGGAAAATTGCTATTAAGATTTTGGTACACTCTTTATTCAGC
ATGCTTATCATGTGCACTATTTTGACCAACTGTGTATTTATGACATTGAG
CAATCCTCCTGACTGGACGAAGAATGTAGAGTACACATTCACTGGATCT
ATACCTTTGAGTCACTTATAAAGATCTTGGCCAGAGGATTCTGCTTAGAA
GATTTCACATTTCTTCGTGACCCATGGAACTGGCTGGATTTCAGTGTCAT
CGTGATGGCATATGTGACAGAGTTTGTGGACCTGGGCAATGTCTCAGCGC
TGAGAACGTTCAGAGTTCTCCGAGCATTGAAAACAATATCAGTCATTCCA
GGTTTAAAGACCATCGTGGGGGCCCTGATCCAGTCGGTGAAGAAGCTGTC
TGACGTCATGATACTCACTGTGTTCTGTCTGAGCGTCTTTGCTCTCATCG
GGCTGCAGCTCTTCATGGGCAACCTGAGGAATAAATGCTTGCAGTGGCCT
CCAAGCGATTCTGCTTTTGAGATCAACACTACTTCCTACTTCAATGGCAC
AATGGACTCAAATGGGACATTTGTTAATGTAACAATGAGCACATTCAACT
GGAAGGACTATATCGCAGATGACAGCCACTTTTATGTTTTGGATGGACAA
AAAGATCCTTTACTTTGTGGAAATGGGTCCGATGCAGGACAATGTCCAGA
AGGGTACATCTGTGTGAAGGCTGGACGAAACCCCAACTACGGTTACACGA
GCTTTGACACATTTAGCTGGGCCTTCTTATCGCTGTTTCGACTCATGACT
CAAGACTACTGGGAGAACCTTTACCAGTTGACATTACGTGCAGCTGGGAA
AACCTACATGATCTTTTTTCGTCCTGGTAATTTTCTTGGGCTCATTTTATT
TGGTGAACTTGATCCTGGCTGTGGTGGCCATGGCCTATGAGGAACAAAAT
CAGGCCACACTGGAGGAGGCTGAGCAGAAAGAGGCGGAGTTTCAGCAGAT
GTTGGAGCAGTTGAAAAAGCAGCAAGAGGAGGCTCAGGCGGTGGCAGCTG
CCTCAGCAGCGTCCAGAGACTTCAGTGGGATAGGAGGGTTAGGAGAACTT
CTGGAGAGTTCTTCAGAAGCTTCCAAGTTGAGCTCCAAGAGTGCCAAGGA
GTGGAGGAATCGGAGGAAGAAGAGGAGACAGAGGGAGCACTTGGAGGGAA

FIG. 5

ACCACAGACCCGAAGGAGACAGGTTTCCCAAGTCGGAATCAGAAGACAGC
GTCAAGCGAAGGAGTTTCCTGTTCTCCCTGGATGGGAACCCGCTGAGCGG
CGACAAGAAGCTGTGTGCTCTCCCCATCAGTCTCTCTTGAGTATCCGTGGCT
CCCTGTTTTTCCCCAAGACGCAATAGCAAAACGAGCATTTTCAGCTTCAGA
GGTCGGGCGAAGGACGTGGGGTCTGAGAATGACTTTGCGGATGATGAACA
CAGCACCTTTGAAGATAGCGAGAGCAGGAGACTCACTGTTTGTGCCGC
ACAGACCTGGAGAGCGACGCAACAGTAACGTTAGTCAGGCCAGTATGTCA
TCCAGGATGGTGCCAGGGCTTCCAGCCAATGGGAAGATGCACAGCACTGT
GGATTGCAATGGTGTGGTTTCCTTGGGTACCACCACTGAAACAGAAGTCA
GGAAGAGAAGGCTAAGTTCTTACCAGATCTCGATGGAAATGCTGGAGGAT
TCCTCTGGGAGACAAAGAGCCATGAGCCAGTATCCTGACCAACAC
GATGGAGGAACTTGAAGAATCTAGACAGAAGTGTCCACCATGCTGGTATA
GATTTGCCAATGTGTTTTTGATCTGGGACTGTTGTGATTCATGGTTGAAA
GTAAAGCATCTTGTGAATTTGATTGTGATGGATCCATTTGTTGACCTGGC
CATCACCATCTGCATCGTGTTAAACACACTGTTCATGGCCATGGAGCACT
ACCCGATGACGGAGCAGTTCAGCAGTGTGCTGACGGTGGGAAACCTGGTC
TTCACCGGGATCTTCACAGCCGAGATGGTCCTGAAAATCATCGCAATGGA
TCCCTATTACTATTTCCAAGAGGGCTGGAATATCTTTGATGGAATTATTG
TTAGCCTGAGTTTAATGGAGCTTGGCCTGGCAAACGTGGAGGGGCTGTCC
GTGCTTCGGTCCTTCAGACTGCTGCGAGTCTTCAAGTTGGCAAAATCCTG
GCCCACACTGAATATGCTCATTAAGATCATCGGCAACTCGGTGGGCGCAC
TGGGCAACCTGACCCTGGTGCTGGCCATCATCGTCTTCATTTTTGCCGTG
GTCGGCATGCAGCTGTTTGGAAAGAGCTACAAGGAGTGTGTTTGCAAGAT
CAATGAGGACTGCAAGCTCCCGCGCTGGCACATGAACGACTTCTTCCACT
CCTTCCTGATAGTGTTCCGCGTGCTGTGGGGAGTGGATAGAGACCATG
TGGGACTGCATGGAGGTCGCGGGCCAGACCATGTGCCTTATTGTGTTTAT
GTTGGTCATGGTGATTGGGAACCTTGTGGTTCTGAACCTCTTCCTGGCCT
TATTGTTGAGTTCCTTTAGTTCAGACAACCTTGCTGCTACGGACGATGAT
AACGAAATGAACACAACCTCCAGATCGCGGTGGGAAGGATGCAAAAGGGAT
TGATTATGTGAAAAATAAGATACGGGAGTGCTTCCGAAAAAGCGTTTTTTA
GAAAGCCGAAAGTGATAGAAATCCACGAAGGGAACAAAATAGACAGCTGC
ATGTCCAATAACACGGGCGTAGTTGAAATAAGCAAAGAGCTTAACTACCT
TAAAGACGGTAACGGAACCACCAGTGGCGTGGGTACTGGAAGCAGTGTGG

FIG. 5

AGAAATACGTAATTGATGAAAATGACTACATGTCATTCATCAACAACCCC
AGCCTCACCGTGACGGTGCCAATTGCCGTGGGAGAGTCTGACTTTGAAAA
TTTAAACACGGAAGAGTTTAGCAGTGAGTCAGAACTGGAAGAAAGCAAGG
AGAAATTAAATGCAACCAGCTCTTCTGAAGGAAGCACAGTTGACGTTGCT
CCGCCCCGAGAAGGTGAACAAGCTGAAATTGAACCTGAGGAGGACCTTAA
GCCAGAAGCTTGCTTTACTGAAGGATGCATTAAAAAATTTCCCTTCTGCC
AAGTAAGTACGGAAGAAGGTAAAGGAAAAATCTGGTGGAATCTTAGGAAG
ACCTGCTATAGCATTGTGGAACACAACTGGTTTGAGACGTTCATTGTGTT
CATGATTCTCCTCAGTAGTGGTGCTTTGGCCTTTGAAGATATATACATTG
AGCAACGGAAGACCATCAAAACCATGCTGGAGTATGCTGACAAAGTCTTC
ACTTACATCTTCATCCTGGAAATGCTCCTCAAATGGGTGGCCTATGGATT
TCAAACCTATTTCACCAATGCCTGGTGCTGGTTGGACTTCTTGATTGTTG
ATGTTTCTTTTGGTTAGCCTGGTGGCCAACGCTCTTGGCTATTCAGAACTT
GGTGCCATCAAATCCCTACGGACCCTGAGAGCTCTGAGGCCGCTCCGAGC
CTTATCCCGCTTTGAAGGCATGAGGGTGGTTGTGAACGCTCTTGTTGGTG
CAATCCCCTCCATCATGAATGTGCTACTGGTGTGCCTCATCTTCTGGTTA
ATCTTTAGTATCATGGGTGTGAATCTGTTTGCTGGAAAGTTCTATCACTG
TGTTAACATGACAACGGGCAGCATGTTCGACATGAGTGAAGTCAACAATT
TCAGCGACTGTCAGGCTCTTGGCAAGCAAGCCCGATGGAAGAATGTGAAA
GTCAACTTTGACAATGTTGGGGCTGGCTACCTGGCATTGCTGCAAGTGGC
CACATTCAAAGGCTGGATGGATATTATGTATGCAGCTGTGGATTCACGGG
ACGTCAAACTGCAGCCTGTATATGAAGAAAAATCTGTACATGTATCTGTAC
TTTGTCATCTTCATCATCTTTGGGTCGTTCTTCACTCTAAATCTATTCAT
CGGCGTCATCATAGACAACTTCAACCAGCAGAAGAAGAAGTTTGGAGGTC
AAGACATCTTTATGACAGAAGAGCAGAAAAAGTACTACAATGCAATGAAG
AAACTTGGCTCCAAAAAACCTCAGAAGCCCATCCCTCGACCTGCAAACAA
ATTTCAAGGAATGGTCTTTGACTTTGTAACCAGACAAGTGTTTGACATCA
GCATCATGATCCTCATCTGCCTCAACATGGTGACCATGATGGTGGAAACG
GACGACCAGAGCAAATACATGACCCTGGTTTTGTCCCGAATCAACCTGGT
ATTCATCGTCCTCTTCACTGGGGAGTTTCTGCTGAAGCTCATCTCTCTCA
GATACTACTACTTCACGATTGGCTGGAACATCTTTGACTTTGTGGTGGTG
ATTCTCTCAATTGTAGGAATGTTCCTTGCTGAGCTGATAGAGAAGTATTT
TGTGTCTCCTACCCTGTTCCGAGTCATCCGCCTGGCCAGGATTGGACGAA
TCCTACGCCTGATCAAAGGCGCCAAGGGGATCCGCACGCTGCTCTTTGCT

FIG. 5

CTGATGATGTCCCTTCCTGCGCTGTTCAACATCGGCCTCCTGCTTTTCCT
CGTCATGTTCATCTACGCCATCTTTGGGATGTCCAACTTTGCCTATGTTA
AAAAAGAGGCTGGAATTGATGACATGTTCAACTTTGAGACTTTTGGCAAC
AGCATGATCTGCCTGTTCCAAATCACCACCTCTGCGGGCTGGGATGGACT
GTTGGCCCCCATCCTCAACAGTGCACCTCCTGACTGTGACCCTGATGCAA
TTCACCCTGGAAGCTCAGTGAAGGGAGACTGTGGGAACCCATCTGTGGGG
ATTTTCTTTTTTTGTCAGCTACATCATCATATCCTTCCTGGTTGTGGTGAA
CATGTACATTGCTGTCATCCTGGAGAACTTCAGCGTTGCCACAGAAGAAA
GTGCAGAGCCCCTGAGTGAGGACGACTTTGAGATGTTCTACGAGGTCTGG
GAGAAGTTCGACCCTGACGCCACCCAGTTCATAGAGTTCTGCAAGCTCTC
TGACTTTGCAGCTGCCCTGGATCCTCCCCTCCTCATCGCAAAGCCAAACA
AAGTCCAGCTCATTGCCATGGACCTGCCCATGGTGAGTGGAGACCGCATC
CACTGCCTGGACATCTTATTTGCTTTTTACAAAGCGGGTCCTGGGTGAGAG
TGGAGAGATGGATGCCCTTCGAATCCAGATGGAAGATCGGTTCATGGCTT
CCAATCCCTCCAAGGTCTCTTATGAGCCCATTACCACCACTCTGAAGCGC
AAACAAGAGGAGGTGTCTGCTGCTATCATTCAGCGTAATTACAGATGTTA
TCTTTTAAAGCAAAGGTTAAAAAACATATCAAATACGTATGACAAAGAGA
CAATCAAGGGGAGGATTGTCTTGCCTATAAAAGGAGATATGGTTATTGAC
AAATTAAATGGGAATTCCACCCCAGAAAAGACAGATGGGAGTTCCTCTAC
CACCTCCCCTCCTTCCTATGACAGTGTAACAAAACCAGATAAGGAAAAGT
TTGAGAAAGACAAACCAGAAAAAGAAAGCAAAGGGAAAGAGGTCTGA

FIG. 5

SEQ ID NO:2

MAQALLVPPGPESFRLFTRESLAAIEKRAAEEKAKKPKKEQDIDDENKPK
PNSDLEAGKNLPFIYGDIPPEMVSEPLEDLDPYYVSKKTFVVLNKGKAIF
RFSATSALYILTPLNPVRKIAIKILVHSLFSMLIMCTILTNCVFMTLSNP
PDWTKNVEYTFTGIYTFESLIKILARGFCLEDFTFLRDPWNWLDFSVIVM
AYVTEFVDLGNVSALRTFRVLRALKTISVIPGLKTIVGALIQSVKKLSDV
MILTVFCLSVFALIGLQLFMGNLRNKCLQWPPSDSAFEINTTSYFNGTMD
SNGTFVNVTMSTFNWKDYIADDSHFYVLDGQKDPLLCGNGSDAGQCPEGY
ICVKAGRNPNYGYTSFDTFSWAFLSLFRLMTQDYWENLYQLTLRAAGKTY
MIFFVLVIFLGSFYLVNLILAVVAMAYEEQNQATLEEAEQKEAEFQQMLE
QLKKQQEEAQAVAAASAASRDFSGIGGLGELLESSSEASKLSSKSAKEWR
NRRKKRRQREHLEGNHRPEGDRFPKSESEDSVKRRSFLFSLDGNPLSGDK
KLCSPHQSLLSIRGSLFSPRRNSKTSIFSFRGRAKDVGSENDFADDEHST
FEDSESRRDSLFVPHRPGERRNSNVSQASMSSRMVPGLPANGKMHSTVDC
NGVVSLGTTTETEVRKRRLSSYQISMEMLEDSSGRQRAMSIASILTNTME
ELEESRQKCPPCWYRFANVFLIWDCCDSWLKVKHLVNLIVMDPFVDLAIT
ICIVLNTLFMAMEHYPMTEQFSSVLTVGNLVFTGIFTAEMVLKIIAMDPY
YYFQEGWNIFDGIIVSLSLMELGLANVEGLSVLRSFRLLRVFKLAKSWPT
LNMLIKIIGNSVGALGNLTLVLAIIVFIFAVVGMQLFGKSYKECVCKINE
DCKLPRWHMNDFFHSFLIVFRVLCGEWIETMWDCMEVAGQTMCLIVFMLV
MVIGNLVVLNLFLALLLSSFSSDNLAATDDDNEMNNLQIAVGRMQKGIDY
VKNKIRECFRKAFFRKPKVIEIHEGNKIDSCMSNNTGVVEISKELNYLKD
GNGTTSGVGTGSSVEKYVIDENDYMSFINNPSLTVTVPIAVGESDFENLN
TEEFSSESELEESKEKLNATSSSEGSTVDVAPPREGEQAEIEPEEDLKPE
ACFTEGCIKKFPFCQVSTEEGKGKIWWNLRKTCYSIVEHNWFETFIVFMI
LLSSGALAFEDIYIEQRKTIKTMLEYADKVFTYIFILEMLLKWVAYGFQT
YFTNAWCWLDFLIVDVSLVSLVANALGYSELGAIKSLRTLRALRPLRALS
RFEGMRVVVNALVGAIPSIMNVLLVCLIFWLIFSIMGVNLFAGKFYHCVN
MTTGSMFDMSEVNNFSDCQALGKQARWKNVKVNFDNVGAGYLALLQVATF

FIG. 5

KGWMDIMYAAVDSRDVKLQPVYEENLYMYLYFVIFIIFGSFFTLNLFIGV
IIDNFNQQKKKFGGQDIFMTEEQKKYYNAMKKLGSKKPQKPIPRPANKFQ
GMVFDFVTRQVFDISIMILICLNMVTMMVETDDQSKYMTLVLSRINLVFI
VLFTGEFLLKLISLRYYYFTIGWNIFDFVVVILSIVGMFLAELIEKYFVS
PTLFRVIRLARIGRILRLIKGAKGIRTLLFALMMSLPALFNIGLLLFLVM
FIYAIFGMSNFAYVKKEAGIDDMFNFETFGNSMICLFQITTSAGWDGLLA
PILNSAPPDCDPDAIHPGSSVKGDCGNPSVGIFFFVSYIIISFLVVVNMY
IAVILENFSVATEESAEPLSEDDFEMFYEVWEKFDPDATQFIEFCKLSDF
AAALDPPLLIAKPNKVQLIAMDLPMVSGDRIHCLDILFAFTKRVLGESGE
MDALRIQMEDRFMASNPSKVSYEPITTTLKRKQEEVSAAIIQRNYRCYLL
KQRLKNISNTYDKETIKGRIVLPIKGDMVIDKLNGNSTPEKTDGSSSTTS
PPSYDSVTKPDKEKFEKDKPEKESKGKEV

SEQ ID NO:3

TGAAAAGATGGCCCAGGCACTGCTGGTACCCCCGGGACCTGAGAGCTTCC
GCCTTTTCACTCGAGAATCTCTTGCTGCTATCGAAAAGCGTGCTGCAGAA
GAGAAAGCCAAGAAACCCAAGAAAGAACAAGACATTGACGATGAGAACAA
GCCAAAGCCAAACAGTGACTTGGAAGCTGGGAAGAACCTTCCATTTATCT
ATGGAGACATTCCTCCAGAGATGGTGTCGGAGCCTCTGGAGGACCTGGAC
CCCTACTACGTCAGTAAGAAAACTTTTGTAGTGTTGAATAAAGGGAAGGC
AATTTTTCGATTCAGTGCCACCTCCGCCTTGTATATTTTAACTCCACTAA
ACCCCGTTAGGAAAATTGCTATTAAGATTTTGGTACACTCTTTATTCAGC
ATGCTTATCATGTGCACTATTTTGACCAACTGTGTATTTATGACATTGAG
CAATCCTCCTGACTGGACGAAGAATGTAGAGTACACATTCACTGGGATCT
ATACCTTTGAGTCACTTATAAAGATCTTGGCCAGAGGATTCTGCTTAGAA
GATTTCACATTTCTTCGTGACCCATGGAACTGGCTGGATTTCAGTGTCAT
CGTGATGGCATATGTGACAGAGTTTGTGGACCTGGGCAATGTCTCAGCGC
TGAGAACGTTCAGAGTTCTCCGAGCATTGAAAACAATATCAGTCATTCCA
GGTTTAAAGACCATCGTGGGGGCCCTGATCCAGTCGGTGAAGAAGCTGTC

FIG. 5

TGACGTCATGATACTCACTGTGTTCTGTCTGAGCGTCTTTGCTCTCATCG
GGCTGCAGCTCTTCATGGGCAACCTGAGGAATAAATGCTTGCAGTGGCCT
CCAAGCGATTCTGCTTTTTGAGATCAACACTACTTCCTACTTCAATGGCAC
AATGGACTCAAATGGGACATTTGTTAATGTAACAATGAGCACATTCAACT
GGAAGGACTATATCGCAGATGACAGCCACTTTTATGTTTTGGATGGACAA
AAAGATCCTTTACTTTGTGGAAATGGGTCCGATGCAGGACAATGTCCAGA
AGGGTACATCTGTGTGAAGGCTGGACGAAACCCCAACTACGGTTACACGA
GCTTTGACACATTTAGCTGGGCCTTCTTATCGCTGTTTCGACTCATGACT
CAAGACTACTGGGAGAACCTTTACCAGTTGACATTACGTGCAGCTGGGAA
AACCTACATGATCTTTTTCGTCCTGGTAATTTTCTTGGGCTCATTTTATT
TGGTGAACTTGATCCTGGCTGTGGTGGCCATGGCCTATGAGGAACAAAAT
CAGGCCACACTGGAGGAGGCTGAGCAGAAAGAGGCGGAGTTTCAGCAGAT
GTTGGAGCAGTTGAAAAAGCAGCAAGAGGAGGCTCAGGCGGTGGCAGCTG
CCTCAGCAGCGTCCAGAGACTTCAGTGGGATAGGAGGGTTAGGAGAACTT
CTGGAGAGTTCTTCAGAAGCTTCCAAGTTGAGCTCCAAGAGTGCCAAGGA
GTGGAGGAATCGGAGGAAGAAGAGGAGACAGAGGAGCACTTGGAGGGAA
ACCACAGACCCGAAGGAGACAGGTTTCCCAAGTCGGAATCAGAAGACAGC
GTCAAGCGAAGGAGTTTCTTCCTGTTCTCCCTGGATGGGAACCCGCTGAGCGG
CGACAAGAAGCTGTGCTCTCCCCATCAGTCTCTCTTGAGTATCCGTGGCT
CCCTGTTTTCCCCAAGACGCAATAGCAAAACGAGCATTTTCAGCTTCAGA
GGTCGGCGAAGGACGTGGGGTCTGAGAATGACTTTGCGGATGATGAACA
CAGCACCTTTGAAGATAGCGAGAGGAGACTCACTGTTTGTGCCGC
ACAGACCTGGAGAGCGACAACAGTAACGTTAGTCAGGCCAGTATGTCA
TCCAGGATGGTGCCAGGGCTTCCAGCCAATGGGAAGATGCACAGCACTGT
GGATTGCAATGGTGTGGTTTCCTTGGGTACCACCACTGAAACAGAAGTCA
GGAAGAGAAGGCTAAGTTCTTACCAGATCTCGATGGAAATGCTGGAGGAT
TCCTCTGGGAGACAAAGAGCCATGAGCATAGCCAGTATCCTGACCAACAC
GATGGAGGAACTTGAAGAATCTAGACAGAAGTGTCCACCATGCTGGTATA
GATTTGCCAATGTGTTTTTTGATCTGGGACTGTTGTGATTCATGGTTGAAA
GTAAAGCATCTTGTGAATTTGATGATGGATCCATTTGTTGACCTGGC
CATCACCATCTGCATCGTGTTAAACACACTGTTCATGGCCATGGAGCACT
ACCCGATGACGGAGCAGTTCAGCAGTGTGCTGACGGTGGGAAACCTGGTC
TTCACCGGGATCTTCACAGCCGAGATGGTCCTGAAAATCATCGCAATGGA
TCCCTATTACTATTTCCAAGAGGGCTGGAATATCTTTGATGGAATTATTG

FIG. 5

TTAGCCTGAGTTTAATGGAGCTTGGCCTGGCAAACGTGGAGGGGCTGTCC
GTGCTTCGGTCCTTCAGACTGCTGCGAGTCTTCAAGTTGGCAAAATCCTG
GCCCACACTGAATATGCTCATTAAGATCATCGGCAACTCGGTGGGCGCAC
TGGGCAACCTGACCCTGGTGCTGGCCATCATCGTCTTCATTTTTGCCGTG
GTCGGCATGCAGCTGTTTGGAAAGAGCTACAAGGAGTGTGTTTGCAAGAT
CAATGAGGACTGCAAGCTCCCGCGCTGGCACATGAACGACTTCTTCCACT
CCTTCCTGATAGTGTTCCGCGTGCTGTGTGGGGAGTGGATAGAGACCATG
TGGGACTGCATGGAGGTCGCGGGCCAGACCATGTGCCTTATTGTGTTTAT
GTTGGTCATGGTGATTGGGAACCTTGTGGTTCTGAACCTCTTCCTGGCCT
TATTGTTGAGTTCCTTTAGTTCAGACAACCTTGCTGCTACGGACGATGAT
AACGAAATGAACAACCTCCAGATCGCGGTGGGAAGGATGCAAAAGGGGAT
TGATTATGTGAAAAATAAGATACGGGAGTGCTTCCGAAAAGCGTTTTTTA
GAAAGCCGAAAGTGATAGAAATCCACGAAGGGAACAAAATAGACAGCTGC
ATGTCCAATAACACGGGCGTAGTTGAAATAAGCAAAGAGCTTAACTACCT
TAAAGACGGTAACGGAACCACCAGTGGCGTGGGTACTGGAAGCAGTGTGG
AGAAATACGTAATTGATGAAAATGACTACATGTCATTCATTCAACAACCCC
AGCCTCACCGTGACGGTGCCAATTGCCGTGGGAGAGTCTGACTTTGAAAA
TTTAAACACGGAAGAGATTTAGCAGTGAGTCAGAACTGGAAGAAAGCAAGG
AGAAATTAAATGCAACCAGCTCTTCTGAAGGAAGCACAGTTGACGTTGCT
CCGCCCCGAGAAGGTGAACAAGCTGAAATTGAACCTGAGGAGGACCTTAA
GCCAGAAGCTTGCTTTACTGAAGGATGCATTAAAAAATTTCCCTTCTGCC
AAGTAAGTACGGAAGAAGGTAAAGGAAAAATCTGGTGGAATCTTAGGAAG
ACCTGCTATAGCATTGTGGAACACAACTGGTTTGAGACGTTCATTGTGTT
CATGATTCTCCTCAGTAGTGGTGCTTTGGCCTTTGAAGATATATACATTG
AGCAACGGAAGACCATCAAAACCATGCTGGAGTATGCTGACAAAGTCTTC
ACTTACATCTTCATCCTGGAAATGCTCCTCAAATGGGTGGCCTATGGATT
TCAAACCTATTTCACCAATGCCTGGTGCTGGTTGGACTTCTTTGATTGTTG
ATGTTTCTTTGGTTAGCCTGGTGGCCAACGCTCTTGGCTATTCAGAACTT
GGTGCCATCAAATCCCTACGGACCCTGAGAGCTCTGAGGCCGCTCCGAGC
CTTATCCCGCTTTGAAGGCATGAGGGTGGTTGTGAACGCTCTTGTTGGTG
CAATCCCCTCCATCATGAATGTGCTACTGGTGTGCCTCATCTTCTGGTTA
ATCTTTAGTATCATGGGTGTGAATCTGTTTGCTGGAAAGTTCTATCACTG
TGTTAACATGACACAACGGGCAGCATGTTCGACATGAGTGAAGTCAACAATT
TCAGCGACTGTCAGGCTCTTGGCAAGCAAGCCCGATGGAAGAATGTGAAA

FIG. 5

GTCAACTTTGACAATGTTGGGGCTGGCTACCTGGCATTGCTGCAAGTGGC
CACATTCAAAGGCTGGATGGATATTATGTATGCAGCTGTGGATTCACGGG
ACGTCAAACTGCAGCCTGTATATGAAGAAAATCTGTACATGTATCTGTAC
TTTGTCATCTTCATCATCTTTGGGTCGTTCTTCACTCTAAATCTATTCAT
CGGCGTCATCATAGACAACTTCAACCAGCAGAAGAAGTTTGGAGGTC
AAGACATCTTTATGACAGAAGAGCAGAAAAAGTACTACAATGCAATGAAG
AAACTTGGCTCCAAAAAACCTCAGAAGCCCATCCCTCGACCTGCAAACAA
ATTTCAAGGAATGGTCTTTGACTTTGTAACCAGACAAGTGTTTGACATCA
GCATCATGATCCTCATCTGCCTCAACATGGTGACCATGATGGTGGAAACG
GACGACCAGAGCAAATACATGACCCTGGTTTTGTCCCGAATCAACCTGGT
ATTCATCGTCCTCTTCACTGGGGAGTTTCTGCTGAAGCTCATCTCTCTCA
GATACTACTTCACGATTGGCTGGAACATCTTTGACTTTGTGGTGGTG
ATTCTCTCAATTGTAGGAATGTTCCTTGCTGAGCTGATAGAGAAGTATTT
TGTGTCTCCTACCCTGTTCCGAGTCATCCGCCTGGCCAGGATTGGACGAA
TCCTACGCCTGATCAAAGGCGCCAAGGGGATCCGCACGCTGCTCTTTGCT
CTGATGATCTGCCTTCCTTCCTGCGCTGTTCAACATCGGCCTCCTGCTTTTCCT
CGTCATGTTCATCTACGCCATCTTTGGGATGTCCAACTTTGCCTATGTTA
AAAAAGAGGCTGGAATTGATGACATGTTCAACTTTGAGACTTTTGGCAAC
AGCATGATCTGCCTGTTCCAAATCACCACCTCTGCGGGCTGGGATGGACT
GTTGGCCCCCATCCTCCTCAACAGTGCACCTCCTGACTGTGACCCTGATGCAA
TTCACCCTGGAAGCTCAGTGAAGGGAGACTGTGTGGGAACCCATCTGTGGGG
ATTTTTCTTTTTTTGTCAGCTACATCATCATATCCTTCCTGGTTGTGGTGAA
CATGTACATTGCTGTCATCCTGGAGAACTTCAGCGTTGCCACAGAAGAAA
GTGCAGAGCCCCTGAGTGAGGACGACTTTGAGATGTTCTACGAGGTCTGG
GAGAAGTTCGACCCTGACGCCACCCAGTTCTATAGAGTTCTGCAAGCTCTC
TGACTTTGCAGCTGCCCTGGATCCTCCCCTCCTCATCGCAAAGCCAAACA
AAGTCCAGCTCATTGCCATGGACCTGCCCATGGTGAGTGGAGACCGCATC
CACTGCCTGGACATCTTATTTGCTTTTACAAAGCGGGTCCTGGGTGAGAG
TGGAGAGATGGATGCCCTTCGAATCCAGATGGAAGATCGGTTCATGGCTT
CCAATCCCTCCAAGGTCTCTTATGAGCCCATTACCACCACTCTGAAGCGC
AAACAAGAGGAGGTGTCTGCTGCTATCATTCAGCGTAATTACAGATGTTA
TCTTTTAAAGCAAAGGTTAAAAAACATATCAAATACGTATGACAAAGAGA
CAATCAAGGGGAGGATTGTCTTGCCTATAAAGGAGATATGGTTATTGAC
AAATTAAATGGGAATTCCACCCCAGAAAAGACAGATGGGAGTTCCTCTAC

FIG. 5

CACCTCCCCTCCTTCCTATGACAGTGTAACAAAACCAGATAAGGAAAAGT
TTGAGAAAGACAAACCAGAAAAAGAAAGCAAAGGGAAAGAGGTCTGAGAG
AATCAAAAGTAAAAAAACAAAACAAAAAAAATTTCAAAAATTTAAAAAGG
AAACAAAGAAATGTCTTTGTAATCAATTGTTTACAGCCTCTGAAGGTAAA
GTGTCCGTGTCAACTGGACTC

SEQ ID NO:4

Genbank® GI No.: 19923380; Ref No.: NM_006922.2; Homo sapiens sodium channel, voltage-gated, type III, alpha (SCN3A), mRNA

AGCGAAGCGGAGGCATAAGCAGAGAGGATTCTGGAAAGGTCTCTTTGTTTTCTTATCCACAGAGAAAGAA
AGAAAAAAAATTGTAACTAATTTGTAAACCTCTGTGGTCAAAAAAAAAAAAAAAAAAAAGCTGAACAGC
TGCCAGAGGAAGACACGTTATACCCTAACCATCTTGGATGCTGGGCTTTGTTATGCTGTAATTCATAAGG
CTCTGTTTTATCAGAGATTATGGAGCAAGAAAACTGAAGCCAAGCCACATCAAGGTTTGACAGGGATGAG
ATACCTGTCAAGGATTCATAGTAGAGTGGCTTACTGGGAAAGGAGCAAAGAATCTCTTCTAGGGATATTG
TAAGAATAAATGAGATAATTCACAGAAGGGACCTGGAGCTTTTCCGGAAAAAGGTGCTGTGACTATCTAA
GGTAATTCGTATGCAAGAAGCTACACGTAATTAAATGTGCAGGATGAAAAGATGGCACAGGCACTGTTGG
TACCCCCAGGACCTGAAAGCTTCCGCCTTTTTACTAGAGAATCTCTTGCTGCTATCGAAAAACGTGCTGC
AGAAGAGAAAGCCAAGAAGCCCAAAAAGGAACAAGATAATGATGATGAGAACAAACCAAAGCCAAATAGT
GACTTGGAAGCTGGAAAGAACCTTCCATTTATTTATGGAGACATTCCTCCAGAGATGGTGTCAGAGCCCC
TGGAGGACCTGGATCCCTACTATATCAATAAGAAAACTTTTATAGTAATGAATAAAGGAAAGGCAATTTT
CCGATTCAGTGCCACCTCTGCCTTGTATATTTTAACTCCACTAAACCCTGTTAGGAAAATTGCTATCAAG
ATTTTGGTACATTCTTTATTCAGCATGCTTATCATGTGCACTATTTTGACCAACTGTGTATTTATGACCT
TGAGCAACCCTCCTGACTGGACAAAGAATGTAGAGTACACATTCACTGGAATCTATACCTTTGAGTCACT
TATAAAAATCTTGGCAAGAGGGTTTTGCTTAGAAGATTTTACGTTTCTTCGTGATCCATGGAACTGGCTG
GATTTCAGTGTCATTGTGATGGCATATGTGACAGAGTTTGTGGACCTGGGCAATGTCTCAGCGTTGAGAA
CATTCAGAGTTCTCCGAGCACTGAAAACAATTTCAGTCATTCCAGGTTTAAAGACCATTGTGGGGGCCCT
GATCCAGTCGGTAAAGAAGCTTTCTGATGTGATGATCCTGACTGTGTTCTGTCTGAGCGTGTTTGCTCTC
ATTGGGCTGCAGCTGTTCATGGGCAATCTGAGGAATAAATGTTTGCAGTGGCCCCCAAGCGATTCTGCTT
TTGAAACCAACACCACTTCCTACTTTAATGGCACAATGGATTCAAATGGGACATTTGTTAATGTAACAAT
GAGCACATTTAACTGGAAGGATTACATTGGAGATGACAGTCACTTTTATGTTTTGGATGGGCAAAAAGAC

FIG. 5

CCTTTACTCTGTGGAAATGGCTCAGATGCAGGCCAGTGTCCAGAAGGATACATCTGTGTGAAGGCTGGTC
GAAACCCCAACTATGGCTACACAAGCTTTAGCTGGGCTTTCCTGTCTCTATTTCGACTCATCAT
GACTCAAGACTATTGGGAAAATCTTTACCAGTTGACATTACGTGCTGCTGGGAAAACATACATGATATTT
TTTGTCCTGGTCATTTTCTTGGGCTCATTTTATTTGGTGAATTTGATCCTGGCTGTGGTGGCCATGGCCT
ATGAGGAGCAGAATCAGGCCACCTTGGAAGAAGCAGAACAAAAAGAGGCCGAATTTCAGCAGATGCTCGA
ACAGCTTAAAAAGCAACAGGAAGAAGCTCAGGCAGTTGCGGCAGCATCAGCTGCTTCAAGAGATTTCAGT
GGAGTAGGTGGGTTAGGAGAGCTGTTGGAAAGTTCTTCAGAAGCATCAAAGTTGAGTTCCAAAGGTGCTA
AAGAATGGAGGAACCGGAGGAAGAAAAGAAGAGAGCACCTTGAAGGAAACAACAAAGGAGAGAG
AGACAGCTTTCCCAAATCCGAATCTGAAGACAGCGTCAAAAGAAGCAGCTTCCTTTTCTCCATGGATGGA
AACAGACTGACCAGTGACAAAAAATTCTGCTCCCCTCATCAGTCTCTCTTGAGTATCCGTGGCTCCCTGT
TTTCCCCAAGACGCAATAGCAAAACAAGCATTTTCAGTTTCAGAGGTCGGGCAAAGGATGTTGGATCTGA
AAATGACTTTGCTGATGATGAACACAGCACATTTGAAGACGGCGAAAGCAGGAGAGACTCACACTGTTTGTG
CCGCACAGACATGGAGAGCGACGCAACAGTAACGTTAGTCAGGCCAGTATGTCATCCAGGATGGTGCCAG
GGCTTCCAGCAAATGGGAAGATGCACAGCACTGTGGATTGCAATGGTGTGGTTTCCTTGGTGGGTGGACC
TTCAGCTCTAACGTCACCTACTGGACAACTTCCCCCAGAGGGCACCACCACTGAAACGGAAGTCAGAAAG
AGAAGGTTAAGCTCTTACCAGATTTCAATGGAGATGCTGGAGGATTCCTCTGGAAGGCAAAGAGCCGTGA
GCATAGCCAGCATTCTGACCAACACACAATGGAAGAACTTGAAGAATCTAGACAGAAAATGTCCGCCATGCTG
GTATAGATTTGCCAATGTGTTCTTGATCTGGGACTGCTGTGATGCATGGTTAAAAGTAAAACATCTTGTG
AATTTAATTGTTATGGATCCATTTGTTGATCTTGCCATCACTATTTGCATTGTCTTAAATACCCTCTTTA
TGGCCATGGAGCACTACCCCATGACTGAGCAATTCAGTAGTGTGTTGACTGTAGGAAACCTGGTCTTTAC
TGGGATTTTCACAGCAGAAATGGTTCTCAAGATCATTGCCATGGATCCTTATTACTATTTCCAAGAAGGC
TGGAATATCTTTGATGGAATTATTGTCAGCCTCAGTTTAATGGAGCTTGGTCTGTCAAATGTGGAGGGAT
TGTCTGTACTGCGATCATTCAGACTGCTTAGAGTTTTCAAGTTGGCAAAATCCTGGCCCACACTAAATAT
GCTAATTAAGATCATTGGCAATTCTGTGGGGGCTCTAGGAAACCTCACCTTGGTGTTGGCCATCATCGTC
TTCATTTTTGCTGTGGTCGGCATGCAGCTCTTTGGTAAGAGCTACAAAGAATGTGTCTGCAAGATCAATG
ATGACTGTACGCTCCCACGGTGGCACATGAACGACTTCTTCCACTCCTTCCTGATTGTGTTCCGCGTGCT
GTGTGGAGAGTGGATAGAGACCATGTGGGACTGTATGGAGGTCGCTGGCCAAACCATGTGCCTTATTGTT
TTCATGTTGGTCATGGTCATTGGAAACCTTGTGGTTCTGAACCTCTTTCTGGCCTTATTATTGAGTTCAT
TTAGCTCAGACAACCTTGCTGCTACTGATGATGACAATGAAATGAATAATCTGCAGATTGCAGTAGGAAG
AATGCAAAAGGGAATTGATTATGTGAAAAATAAGATGCGGGAGTGTTTCCAAAAAGCCTTTTTTAGAAAG
CCAAAAGTTATAGAAATCCATGAAGGCAATAAGATAGACAGCTGCATGTCCAATAATACTGGAATTGAAA
TAAGCAAAGAGCTTAATTATCTTAGAGATGGGAATGGAACCACCAGTGGTGTAGGTACTGGAAGCAGTGT
TGAAAAATACGTAATCGATGAAAATGATTATATGTCATTCATAAACACCCCAGCCTCACCGTCACAGTG
CCAATTGCTGTTGGAGAGTCTGACTTTGAAAACTTAAATACTGAAGAGTTCAGCAGTGAGTCAGAACTAG

FIG. 5

AAGAAAGCAAAGAGAAATTAAATGCAACCAGCTCATCTGAAGGAAGCACAGTTGATGTTGTTCTACCCCG
AGAAGGTGAACAAGCTGAAACTGAACCCGAAGAAGACTTTAAACCGGAAGCTTGTTTTACTGAAGGGTGT
ATTAAAAAGTTTCCATTCTGTCAAGTAAGTACAGAAGAAGGCAAAGGGAAGATCTGGTGGAATCTTCGAA
AAACCTGCTACAGTATTGTTGAGCACAACTGGTTTGAGACTTTCATGATCCTTCTTCTCAGTAG
TGGTGCATTGGCCTTTGAAGATATATACATTGAACAGCGAAAGACTATCAAACCATGCTAGAATATGCT
GACAAAGTCTTTACCTATATATTCATTCTGGAAATGCTTCTCAAATGGGTTGCTTATGGATTTCAAACAT
ATTTCACTAATGCCTGGTGCTGGCTAGATTTCTTGATCGTTGATGTTTCTTTGGTTAGCCTGGTAGCCAA
TGCTCTTGGCTACTCAGAACTCGGTGCCATCAAATCATTACGGACATTAAGAGCTTTAAGACCTCTAAGA
GCCTTATCCCGGTTTGAAGGCATGAGGGTGGTTGTGAATGCTCTTGTTGGAGCAATTCCCTCTATCATGA
ATGTGCTGTTGGTCTGTCTCATCTTCTGGTTGATCTTTAGCATCATGGGTGTGAATTTGTTTGCTGGCAA
GTTCTACCACTGTGTTTAACATGACAACGGGTAACATGTTTGACATTAGTGATGTTTAACAATTTGAGTGAC
TGTCAGGCTCTTGGCAAGCAAGCTCGGTGGAAAAACGTGAAAGTAAACTTTGATAATGTTGGCGCTGGCT
ATCTTGCACTGCTTCAAGTGGCCACATTTAAAGGCTGGATGGATATTATGTATGCAGCTGTTGATTCACG
AGATGTTAAACTTCAGCCTGTATATGAAGAAAATCTGTACATGTATTTATACTTTGTCATCTTTATCATC
TTTGGGTCATTCTTCACTCTGAATCTATTCATAGATAACTTCCAACCAGCAGAAAAAGA
AGTTTGGAGGTCAAGACATCTTTATGACAGAGGAACAGAAAAAATATTACAATGCAATGAAGAAACTTGG
ATCCAAGAAACCTCAGAAACCCATACCTCGCCCAGCAAACAAATTCCAAGGAATGGTCTTTGATTTTGTA
ACCAGACAAGTCTTTGATATCAGCATCATGATCCTCATCTGCCTCAACATGGTCACCATGATGGTGGAAA
CGGATGACCAGGGCAAATACATGACCCTAGTTTTGTCCCGGATCAACCTAGTGTTCATTGTTCTGTTCAC
TGGAGAATTTGTGCTGAAGCTCGTTTCCCTCAGACACTACTTCACTATAGGCTGGAACATCTTTGAC
TTTGTGGTGGTGATTCTCTCCATTGTAGGTATGTTTCTGGCTGAGATGATATTCTGTGTCCC
CTACCTTGTTCCGAGTGATCCGTCTTGCCAGGATTGGCCGAATCCTACGTCTGATCAAAGGAGCAAAGGG
GATCCGCACGCTGCTCTTTGCTTTGATGATGTCCCTTCCTGCGTTGTTTAACATCGGCCTCCTGCTCTTTC
CTGGTCATGTTTATCTATGCCATCTTTGGGATGTCCAACTTTGCCTATGTTAAAAGGAAGCTGGAATTG
ATGACATGTTCAACTTTGAGACCTTTGGCAACAGCATGATCTGCTTGTTCCAAATTACAACCTCTGCTGG
CTGGGATGGATTGCTAGCACCTATTCTTAATAGTGCACCACCCGACTGTGACCCTGACACAATTCACCCT
GGCAGCTCAGTTAAGGGAGACCGTGGGGACCCATCTGTTGGGATTTTCTTTTTGTCAGTTACATCATCA
TATCCTTCCTGGTTGTGGTGAACATGTACATCGCGGTCATCCTGGAGAACTTCAGTGTTGCTACTGAAGA
AAGTGCAGAGCCCCTGAGTGAGGATGACTTTGAGATGTTCTATGAGGTTTGGGAAAAGTTTGATCCCGAT
GCGACCCAGTTTATAGAGTTCTCTAAACTCTCTGATTTTGCAGCTGCCCTGGATCCTCCTCTTCTCATAG
CAAAACCCAACACAAAGTCCAGCTTATTGCCATGGATCTGCCCATGGTCAGTGGTGACCGGATCCACTGTCT
TGATATTTTATATTTGCCTTTACAAAGCGTGTTTTGTGTGAGAGTGGAGAGATGGATGCCCTTCGAATACAG
ATGGAAGACAGGTTTATGGCATCAAACCCCTCCAAAGTCTCTTATGAGCCTATTACAACCACTTTGAAAAC
GTAAACAAGAGAGGAGGTGTCTGCCGCTATCATTCAGCGTAATTTCAGATGTTATCTTTTTAAAGCAAAGGTT

FIG. 5

AAAAAATATATCAAGTAACTATAACAAAGAGGCAATTAAAGGGAGGATTGACTTACCTATAAAACAAGAC
ATGATTATTGACAAACTAAATGGGAACTCCACTCCAGAAAAAACAGATGGGAGTTCCTCTACCACCCCTC
CTCCTTCCTATGATAGTGTAACAAAACCAGACAAGGAAAAGTTTGAGAAAGACAAACCAGAAAAAGAAAG
CAAAGGAAAAGAGGTCAGAGAAAATCAAAAGTAAAAAGAAACAAAGAATTATCTTTGTGATCAATTGTTT
ACAGCCTATGAAGGTAAAGTATATGTGTCAACTGGACTTCAAGAGGAGGTCCATGCCAAACTGACTGTTT
TAACAAATACTCATAGTCAGTGCCTATACAAGACAGTGAAGTGACCTCTCTGTCACTGCAACTCTGTGAA
GCAGGGTATCAACGTTGACAAGAGGTTGCTGTTTTTATTACCAGCTGACACTGCTGAGGAGAAACCCAAT
GGCTACCTAGACTATAGGGATAGTTGTGCAAAGTGAACATTGTAACTACACCAAACACCTTTAGTACAGT
CCTTGCATCCATTCTATTTTTAACTTCCATATCTGCCATATTTTTACAAAATTTGTTCTAGTGCATTTCC
ATGGTCCCCAATTCATAGTTTATTCATAATGCTATGTCACTATTTTTGTAAATGAGGTTTACGTTGAAGA
AACAGTATACAAGAACCCTGTCTCTCAAATGATCAGACAAAGGTGTTTTGCCAGAGAGATAAAATTTTTG
CTCAAAACCAGAAAAAGAATTGTAATGGCTACAGTTTCAGTTACTTCCATTTTCTAGATGGCTTTAATTT
TGAAAGTATTTTAGTCTGTTATGTTTGTTTCTATCTGAACAGTTATGTGCCTGTAAAGTCTCCTCTAATA
TTTAAAGGATTATTTTTATGCAAAGTATTCTGTTTCAGCAAGTGCAAATTTTATTCTAAGTTTCAGAGCT
CTATATTTAATTTAGGTCAAATGCTTTCCAAAAAGTAATCTAATAAATCCATTCTAGAAAAATATATCTA
AAGTATTGCTTTAGAATAGTTGTTCCACTTTCTGCTGCAGTATTGCTTTGCCATCTTCTGCTCTCAGCAA
AGCTGATAGTCTATGTCAATTAAATACCCTATGTTATGTAAATAGTTATTTTATCCTGTGGTGCATGTTT
GGGCAAATATATATATAGCCTGATAAACAACTTCTATTAAATCAAATATGTACCACAGTGTATGTGTCTT
TTGCAAGCTTCCAACAGGGATGTATCCTGTATCATTCATTAAACATAGTTTAAAGGCTATCACTAATGCA
TGTTAATATTGCCTATGCTGCTCTATTTTACTCAATCCATTCTTCACAAGTCTTGGTTAAAGAATGTCAC
ATATTGGTGATAGAATGAATTCAACCTGCTCTGTCCATTATGTCAAGCAGAATAATTTGAAGCTATTTAC
AAACACCTTTACTTTTGCACTTTTAATTCAACATGAGTATCATATGGTATCTCTCTGGATTTCAAGGAAA
CACACTGGATACTGCCTACTGACAAAACCTATTCTTCATATTTTGCTAAAAATATGTCTAAAACTTGTTT
AAATATAAATAATGTAAAAATATAATCAACTTTATTTGTCAGCATTTTGTACATAAGAAAATTATTTTCA
GGTTGATGACATCACAATTTATTTTACTTTATGCTTTTGCTTTTGATTTTTAATCACAATTCCAAACTTT
TGAATCCATAAGATTTTTCAATGGATAATTTCCTAAAATAAAAGTTAGATAATGGGTTTTATGGATTTCT
TTGTTATAATATATTTTCTACCATTCCAATAGGAGATACATTGGTCAAACACTCAAACCTAGATCATTTT
CTACCAACTATGGTTGCCTCAATATAACCTTTTATTCATAGATGTTTTTTTTTATTCAACTTTTGTAGTA
TTTACGTATGCAGACTAGTCTTATTTTTTTAATTCCTGCTGCACTAAAGCTATTACAAATATAACATGGA
CTTTGTTCTTTTTTAGCCATGAACAAAGTGGCAAAGTTGTGCAATTACCTAACATGATATAAATTTTTGTT
TTTTGCACAAACCAAAAGTTTAATGTTAATTCTTTTTACAAAACTATTTACTGTAGTGTATTGAAGAACT
GCATGCAGGGAATTGCTATTGCTAAAAAGAATGGTGAGCTACGTCATTATTGAGCCAAAAGAATAAATTT
CATTTTTTATTGCATTTCACTTATTGGGCTCTGGGGTTTTTTGTTTTTGTTTTTTGCTGTTGGCAGTTTA
AAATATATATAATTAATAAAACCTGTGCTTGATCTGACATTTGTATACATAAAAGTTTACATGAATTTTA

FIG. 5

CAACAAACTAGTGCATGATTCACCAAGCAGTACTACAGAACAAAGGCAAATTAAAAGCAGCTTTGTGAAC
TTTTATGTGTGCAAAGGATCAAGTTCACATGTTCCAACTTTCAGGTTTGATAATAATAGTAGTAACCACC
TACAATAGCTTTCAATTTCAATTAACTCCCTTGGCTATAAGCATCTAAACTCATCTTCTTTCAATATAAT
TGATGCTATCTCCTAATTACTTGGTGGCTAATAAATGTTACATTCTTTGTTACTTAAATGCATTATATAA
ACTCCTATGTATACATAAGGTATTAATGATATAGTTATTGAGAATTTATATTAACTTTTTTTTCAAGAAC
CCTTGGATTTATGTGAGGTCAAAACCAAACTCTTATTCTCAGTGGAAAACTCCAGTTGTAATGCATATTT
TTAAAGACAATTTGGATCTAAATATGTATTTCATAATTCTCCCATAATAAATTATATAAGGTGGAAAAAA
AAAAAAAAAAAAAAAAAAAAAA

SEQ ID NO:5

GenBank® GI No.:19923381; Ref. No.:NP_008853.2; sodium channel, voltage-gated, type III, alpha; sodium channel, voltage-gated, type III, alpha polypeptide [Homo sapiens]

MAQALLVPPGPESFRLFTRESLAAIEKRAAEEKAKKPKKEQDNDDENKPKPNSDLEAGKNLPFIYGDIPP
EMVSEPLEDLDPYYINKKTFIVMNKGKAIFRFSATSALYILTPLNPVRKIAIKILVHSLFSMLIMCTILT
NCVFMTLSNPPDWTKNVEYTFTGIYTFESLIKILARGFCLEDFTFLRDPWNWLDFSVIVMAYVTEFVDLG
NVSALRTFRVLRALKTISVIPGLKTIVGALIQSVKKLSDVMILTVFCLSVFALIGLQLFMGNLRNKCLQW
PPSDSAFETNTTSYFNGTMDSNGTFVNVTMSTFNWKDYIGDDSHFYVLDGQKDPLLCGNGSDAGQCPEGY
ICVKAGRNPNYGYTSFDTFSWAFLSLFRLMTQDYWENLYQLTLRAAGKTYMIFFVLVIFLGSFYLVNLIL
AVVAMAYEEQNQATLEEAEQKEAEFQQMLEQLKKQQEEAQAVAAASAASRDFSGVGGLGELLESSSEASK
LSSKGAKEWRNRRKKRRQREHLEGNNKGERDSFPKSESEDSVKRSSFLFSMDGNRLTSDKKFCSPHQSLL
SIRGSLFSPRRNSKTSIFSFRGRAKDVGSENDFADDEHSTFEDGESRRDSLFVPHRHGERRNSNVSQASM
SSRMVPGLPANGKMHSTVDCNGVVSLVGGPSALTSPTGQLPPEGTTTETEVRKRRLSSYQISMEMLEDSS
GRQRAVSIASILTNTMEELEESRQKCPPCWYRFANVFLIWDCCDAWLKVKHLVNLIVMDPFVDLAITICI
VLNTLFMAMEHYPMTEQFSSVLTVGNLVFTGIFTAEMVLKIIAMDPYYYFQEGWNIFDGIIVSLSLMELG
LSNVEGLSVLRSFRLLRVFKLAKSWPTLNMLIKIIGNSVGALGNLTLVLAIIVFIFAVVGMQLFGKSYKE
CVCKINDDCTLPRWHMNDFFHSFLIVFRVLCGEWIETMWDCMEVAGQTMCLIVFMLVMVIGNLVVLNLFL
ALLLSSFSSDNLAATDDDNEMNNLQIAVGRMQKGIDYVKNKMRECFQKAFFRKPKVIEIHEGNKIDSCMS
NNTGIEISKELNYLRDGNGTTSGVGTGSSVEKYVIDENDYMSFINNPSLTVTVPIAVGESDFENLNTEEF
SSESELEESKEKLNATSSSEGSTVDVVLPREGEQAETEPEEDFKPEACFTEGCIKKFPFCQVSTEEGKGK

FIG. 5

IWWNLRKTCYSIVEHNWFETFIVFMILLSSGALAFEDIYIEQRKTIKTMLEYADKVFTYIFILEMLLKWV
AYGFQTYFTNAWCWLDFLIVDVSLVSLVANALGYSELGAIKSLRTLRALRPLRALSRFEGMRVVVNALVG
AIPSIMNVLLVCLIFWLIFSIMGVNLFAGKFYHCVNMTTGNMFDISDVNNLSDCQALGKQARWKNVKVNF
DNVGAGYLALLQVATFKGWMDIMYAAVDSRDVKLQPVYEENLYMYLYFVIFIIFGSFFTLNLFIGVIIDN
FNQQKKKFGGQDIFMTEEQKKYYNAMKKLGSKKPQKPIPRPANKFQGMVFDFVTRQVFDISIMILICLNM
VTMMVETDDQGKYMTLVLSRINLVFIVLFTGEFVLKLVSLRHYYFTIGWNIFDFVVVILSIVGMFLAEMI
EKYSVSPTLFRVIRLARIGRILRLIKGAKGIRTLLFALMMSLPALFNIGLLLFLVMFIYAIFGMSNFAYV
KKEAGIDDMFNFETFGNSMICLFQITTSAGWDGLLAPILNSAPPDCDPDTIHPGSSVKGDRGDPSVGIFF
FVSYIIISFLVVVNMYIAVILENFSVATEESAEPLSEDDFEMFYEVWEKFDPDATQFIEFSKLSDFAAAL
DPPLLIAKPNKVQLIAMDLPMVSGDRIHCLDILFAFTKRVLCESGEMDALRIQMEDRFMASNPSKVSYEP
ITTTLKRKQEEVSAAIIQRNFRCYLLKQRLKNISSNYNKEAIKGRIDLPIKQDMIIDKLNGNSTPEKTDG
SSSTTPPPSYDSVTKPDKEKFEKDKPEKESKGKEVRENQK

SEQ ID NO:6

GenBank® GI No.: 12642271; GB No.:AF225986.1; Homo sapiens voltage-gated sodium channel alpha subunit splice variant SCN3A-s (SCN3A) mRNA, complete cds, alternatively spliced

AGCGAAGCGGAGGCATAAGCAGAGAGGATTCTGGAAAGGTCTCTTTGTTTTCTTATCCACAGAGAAAGAA
AGAAAAAAAATTGTAACTAATTTGTAAACCTCTGTGGTCAAAAAAAAAAAAAAAAAAAAAGCTGAACAGC
TGCCAGAGGAAGACACGTTATACCCTAACCATCTTGGATGCTGGGCTTTGTTATGCTGTAATTCATAAGG
CTCTGTTTTATCAGAGATTATGGAGCAAGAAAACTGAAGCCAAGCCACATCAAGGTTTGACAGGGATGAG
ATACCTGTCAAGGATTCATAGTAGAGTGGCTTACTGGGAAAGGAGCAAAGAATCTCTTCTAGGGATATTG
TAAGAATAAATGAGATAATTCACAGAAGGGACCTGGAGCTTTTCCGGAAAAAGGTGCTGTGACTATCTAA
GGTAATTCGTATGCAAGAAGCTACACGTAATTAAATGTGCAGGATGAAAAGATGGCACAGGCACTGTTGG
TACCCCCAGGACCTGAAAGCTTCCGCCTTTTTACTAGAGAATCTCTTGCTGCTATCGAAAAACGTGCTGC
AGAAGAGAAAGCCAAGAAGCCCAAAAAGGAACAAGATAATGATGATGAGAACAAACCAAAGCCAAATAGT
GACTTGGAAGCTGGAAAGAACCTTCCATTTATTTATGGAGACATTCCTCCAGAGATGGTGTCAGAGCCCC
TGGAGGACCTGGATCCCTACTATATCAATAAGAAAACTTTTATAGTAATGAATAAAGGAAAGGCAATTTT
CCGATTCAGTGCCACCTCTGCCTTGTATATTTTAACTCCACTAAACCCTGTTAGGAAAATTGCTATCAAG

FIG. 5

ATTTTGGTACATTCTTTATTCAGCATGCTTATCATGTGCACTAATTTTGACCAACTGTGTATTTATGACCT
TGAGCAACCCTCCTGACTGGACAAAGAATGTAGAGTACACATTCACTGGAATCTATACCTTTGAGTCACT
TATAAAAATCTTGGCAAGAGGGTTTTGCTTAGAAGATTTTACGTTTCTTCGTGATCCATGGAACTGGCTG
GATTTCAGTGTCATTGTGATGGCATATGTGACAGAGTTTGTGGACCTGGGCAATGTCTCAGCGTTGAGAA
CATTCAGAGTTCTCCGAGCACTGAAAACAATTTCAGTCATTCCAGGTTTAAAGACCATTGTGGGGGCCCT
GATCCAGTCGGTAAAGAAGCTTTCTGATGTGTTCTGACTGTGTTCTGAGCGTGTTTGCTCTC
ATTGGGCTGCAGCTGTTCATGGGCAATCTGAGGAATAAATGTTTGCAGTGGCCCCCAAGCGATTCTGCTT
TTGAAACCAACACCACTTCCTACTTTAATGGCACAATGGGACATTTGTTAATGTAACAAT
GAGCACATTTAACTGGAAGGATTACATTGGAGATGACAGTCACTTTATGTTTTGGATGGGCAAAAAGAC
CCTTTACTCTGTGGAAATGGCTCAGATGCAGGCCAGTGTCCAGAAGGATACATCTGTGTGAAGGCTGGTC
GAAACCCCAACTATGGCTACACAAGCTTTGACACCTTTAGCTGGGCTTTCCTGTCTCTATTTCGACTCAT
GACTCAAGACTATTGGGAAAATCTTTACCAGTTGACATTACGTGCTGCTGGGAAAACATACATGATATTT
TTTGTCCTGGTCATTTTCTTGGGCTCATTTTATTTGGTGAATTTGATCCTGGCTGTGGTGGCCATGGCCT
ATGAGGAGCAGAATCAGGCCACCTTGGAAGAAGCAGAACAAAAAGAGGCCGAATTTCAGCAGATGCTCGA
ACAGCTTAAAAAGCAACAGGAAGAAGCTCAGGCAGTTGCGGCAGCATCAGCTGCTTCAAGAGATTTCAGT
GGAGTAGGTGGGTTAGGAGAGCTGTTGGAAAGTTCTTCAGAAGCATCAAAGTTGAGTTCCAAAGGTGCTA
AAGAATGGAGGAACCGGAGGAAGAAAAGAAGACAGAGAGAGCACCTTGAAGGAAACAACAAAGGAGAGAG
AGACAGCTTTCCCAAATCCGAATCTGAAGACAGCGTCAAAAGAAGCAGCTTCCTTTTCTCCATGGATGGA
AACAGACTGACCAGTGACAAAAAATTCTGCTCCCCTCATCAGTCTCTCTTGAGTATCCGTGGCTCCCTGT
TTTCCCCAAGACGCAATAGCAAAACAAGCATTTTCAGTTTCAGAGGTCGGGCAAAGGATGTTGGATCTGA
AAATGACTTTGCTGATGATGAACACAGCACATTTGAAGACAGCGAAAGCAGGAGAGACTCACTGTTTGTG
CCGCACAGACATGGAGAGCGACGCAACACATGTAACGGAAACGGAAGTCAGAAAGAGAAGGT
TAAGCTCTTACCAGATTTCAATGGAGATGCTGGAGGATTCCTCTGGAAGGCAAAGAGCCGTGAGCATAGC
CAGCATTCTGACCAACACAATGGAAGAACTTGAAGAATCTAGACAGAAATGTCCGCCATGCTGGTATAGA
TTTGCCAATGTGTTCTTGATCTGGGACTGCTGTGATGCATGGTTAAAAGTAAAACATCTTGTGAATTTAA
TTGTTATGGATCCATTTGTTGATCTTGCCATCACTATTTGCATTGTCTTAAATACCCTCTTTATGGCCAT
GGAGCACTACCCCATGACTGAGCAATTCAGTAGTGTGTTGACTGTAGGAAACCTGGTCTTTACTGGGATT
TTCACAGCAGAAATGGTTCTCAAGATCATTGCCATGGATCCTTATTACTATTTCCAAGAAGGCTGGAATA
TCTTTGATGGAATTATTGTCAGCCTCAGTTTAATGGAGCTTGGTCTGTCAAATGTGGAGGGATTGTCTGT
ACTGCGATCATTCAGACTGCTTAGAGTTTTCAAGTTGGCAAAATCCTGGCCCACACTAAATATGCTAATT
AAGATCATTGGCAATTCTGTGGGGGCTCTAGGAAACCTCACCTTGGTGTTGGCCATCATCGTCTTCATTT
TTGCTGTGGTCGGCATGCAGCTCTTTGGTAAGAGCTACAAAGAATGTGTCTGCAAGATCAATGATGACTG
TACGCTCCCCACGGTGGCACATGAACGACTTCTTCCACTCCTTCCTGATTGTGTTCCGCGTGCTGTGTGGA
GAGTGGATAGAGACCATGTGGACTGTATGGAGGTCGCTGGCCAAACCATGTGCCTTATTGTTTTTCATGT

FIG. 5

TGGTCATGGTCATTGGAAACCTTGTGGTTCTGAACCTCTTTCTGGCCTTATTATTGAGTTCATTTAGCTC
AGACAACCTTGCTGCTACTGATGATGACAATGAAATGAATAATCTGCAGATTGCAGTAGGAAGAATGCAA
AAGGGAATTGATTATATGTGAAAAATAAGATGCGGGAGTGTTTCCAAAAAGCCTTTTTTTAGAAAGCCAAAAG
TTATAGAAATCCATGAAGGCAATAAGATAGACAGCTGCATGTCCAATAATACTGGAATTGAAATAAGCAA
AGAGCTTAATTATCTTAGAGATGGGAATGGAACCACCAGTGGTGTAGGTACTGGAAGCAGTGTTGAAAAA
TACGTAATCGATGAAAAATGATTATATGTCATTCATAAACAACCCCAGCCTCACCGTCACAGTGCCAATTG
CTGTTGGAGAGTCTGACTTTGAAAACTTAAATACTGAAGAGTTCAGCAGTGAGTCAGAACTAGAAGAAAG
CAAAGAGAAATTAAATGCAACCAGCTCATCTGAAGGAAGCACAGTTGATGTTGTTCTACCCCGAGAAGGT
GAACAAGCTGAAACTGAACCCGAAGAAGACTTTAAACCGGAAGCTTGTTTTACTGAAGGGTGTATTAAAA
AGTTTCCATTCTGTCAAGTAAGTACAGAAGAAGGGAAGATCTGGTGGAATCTTCGAAAAACCTG
CTACAGTATTGTTGAGCACAACTGGTTTGAGACTTTCATTGTGTTCATGATCCTTCTCAGTAGTGGTGCA
TTGGCCTTTGAAGATATATACATTGAACAGCGAAAGACTATCAAAACCATGCTAGAATATGCTGACAAAG
TCTTTACCTATATATTCATTCTGGAAATGCTTCTCAAATGGGTTGCTTATGGATTTCAAACATATTTCAC
TAATGCCTGGTGCTGGCTAGATTTCTTGATCGTTGATGTTTCTTTGGTTAGCCTGGTAGCCAATGCTCTT
GGCTACTCAGAACTCGGTGCCATCAAATCATTACGGACATTAAGAGCTTTAAGACCTCTAAGAGCCTTAT
CCCGGTTTGAAGGCATGAGGGTGGTTGTGAATGCTCTTGTTGGAGCAATTCCCTCTATCATGAATGTGCT
GTTGGTCTGTCTCATCTTCTGGTTGATCTTTAGCATCATGGGTGTGAATTTGTTTGCTGGCAAGTTCTAC
CACTGTGTTAACATGACAACGGGTAACATGTTTGACATTAGTGATGTTAACAATTTGAGTGACTGTCAGG
CTCTTGGCAAGCAAGCTCGGTGGAAAAACGTGAAAGTAAACTTTGATAATGTTGGCGCTGGCTATCTTGC
ACTGCTTCAAGTGGCCACATTTAAAGGCTGGATGATATTATGTATGCAGCTGTTGATTCACGAGATGTT
AAACTTCAGCCTGTATATGAAGAAAATCTGTACATGTATTTATACTTTGTCATCTTTATCATCTTTGGGT
CATTCTTCACTCTGAATCTATTCATTGGTGTCATCATAGATAACTTCAACCAGCAGAAAAAGAAGTTTGG
AGGTCAAGACATCTTTATGACAGAGGAACAGAAAAAATATTACAATGCAATGAAGAAACTTGGATCCAAG
AAACCTCAGAAACCCATACCTCGCCCAGCAAACAAATTCCAAGGAATGGTCTTTGATTTTGTAACCAGAC
AAGTCTTTGATATCAGCATCATGATCCTCATCTGCCTCAACATGGTCACCATGATGGTGGAAACGGATGA
CCAGGGCAAATACATGACCCTAGTTTTGTCCCGGATCAACCTAGTGTTCATTGTTCTGTTCACTGGAGAA
TTTGTGCTGAAGCTCGTTTCCCTCAGACACTACTACTTCACTATAGGCTGGAACATCTTTGACTTTGTGG
TGGTGATTCTCTCCATTGTAGGTATGTTTCTGGCTGAGATGATATTCTGTGTCCCCCTACCTTT
GTTCCGAGTGATCCGTCTTGCCAGGATTGGCCGAATCCCTACGTCTGATCAAGGAGCAAGGGGATCCGC
ACGCTGCTCTTTGCTTTGATGATGTCCCTTCCTGCGTTGTTTAACATCGGCCTCCTGCTCTTCCTGGTCA
TGTTTATCTATGCCATCTTTGGGATGTCCAACTTTGCCTATGTTTAAAAGGAAGCTGGAATTGATGACAT
GTTCAACTTTGAGACCTTTGGCAACAGCATGATCTGCTTGTTCCAAATTACAACCTCTGCTGGCTGGGAT
GGATTGCTAGCACCTATTCTTAATAGTGCACCACCCGACTGTGACCCTGACACACAATTCACCCTGGCAGCT
CAGTTAAGGGAGACCGTGGGGACCCATCTGTTGGGATTTTCTTTTTTGTCAGTTACATCATCATATCCTT

FIG. 5

CCTGGTTGTGGTGAACATGTACATCGCGGTCATCCTGGAGAACTTCAGTGTTGCTACTGAAGAAAGTGCA
GAGCCCCTGAGTGAGGATGACTTTGAGATGTTCTATGAGGTTTGGGAAAAGTTTGATCCCGATGCGACCC
AGTTTATAGAGTTCTCTAAACTCTCTGATTTTGCAGCTGCCCTGGATCCTCCTCTTCTCATAGCAAACC
CAACAAAGTCCAGCTTATTGCCATGGATCTGCCCATGGTCAGTGGTGACCGGATCCACTGTCTTGATATT
TTATTTGCCTTTACAAAGCGTGTTTTGTGTGAGAGTGGAGATGCCCTTCGAATACAGATGGAAG
ACAGGTTTATGGCATCAACCCCTCCAAAGTCTCTTATGAGCCTATTACAACCACTTTGAAACGTAAACA
AGAGGAGGTGTCTGCCGCTATCATTCAGCGTAATTTCAGATGTTATCTTTTAAAGCAAAGGTTTAAAAAAT
ATATCAAGTAACTATAACAAAGAGGCAATTAAAGGGAGGATTGACTTACCTATAAAACAAGACATGATTA
TTGACAAACTAAATGGGAACTCCACTCCAGAAAAAACAGATGGGAGTTCCTCTACCACCTCTCCTCCTTC
CTATGATAGTGTTACAAAACCAGACAAGGAAAAGTTTGAGAAAGACAAACCAGAAAAAGAAAGCAAAGGA
AAAGAGGTCAGAGAAAATCAAAAGTAAAAAGAAACAAAGAATTATCTTTGTGATCAATTGTTTACAGCCT
ATGAAGGTAAAGTATATGTGTCAACTGGACTTCAAGAGGAGGTCCATGCCAAACTGACTGTTTTAACAAA
TACTCATAGTCAGTGCCTATACAAGACAGTGAAGTGACCTCTCTGTCACTGCAACTCTGTGAAGCAGGGT
ATCAACGTTGACAAGAGGTTGCTGTTTTTATTACCAGCTGACACTGCTGAGGAGAAACCCAATGGCTACC
TAGACTATAGGGATAGTTGTGCAAAGTGAACATTGTAACTACACCAAACACCTTTAGTACAGTCCTTGCA
TCCATTCTATTTTTAACTTCCATATCTGCCATATTTTTACAAAATTTGTTCTAGTGCATTTCCATGGTCC
CCAATTCATAGTTTATTCATAATGCTATGTCACTATTTTTGTAAATGAGGTTTACGTTGAAGAAACAGTA
TACAAGAACCCTGTCTCTCAAATGATCAGACACAAAGGTGTTTTGCCAGAGAGATAAAATTTTTGCTCAAAA
CCAGAAAAAGAATTGTAATGGCTACAGTTTCAGTTACTTCCATTTTCTAGATGGCTTTAATTTTGAAAGT
ATTTTAGTCTGTTATGTTTGTTTCTATCTGAACAGTTATGTGCCTGTAAAGTCTCCTCTAATATTTAAAG
GATTATTTTTATGCAAAGTATTCTGTTTCAGCAAGTGCAAATTTTATTCTAAGTTTCAGAGCTCTATATT
TAATTTAGGTCAAATGCTTTCCAAAAAGTAATCTAATAAATCCATTCTAGAAAAATATATCTAAAGTATT
GCTTTAGAATAGTTGTTCCACTTTCTGCTGCAGTATTGCTTTGCCATCTTCTGCTCTCAGCAAAGCTGAT
AGTCTATGTCAATTAAATACCCTATGTTATGTAAATAGTTATTTTATCCTGTGGTGCATGTTTGGGCAAA
TATATATATAGCCTGATAAACAACTTCTATTAAATCAAATATGTACCACAGTGTATGTGTCTTTTGCAAG
CTTCCAACAGGGATGTATCCTGTATCATTCATTAAACATAGTTTAAAGGCTATCACTAATGCATGTTAAT
ATTGCCTATGCTGCTCTATTTTACTCAATCCATTCTTCACAAGTCTTGGTTAAAGAATGTCACATATTGG
TGATAGAATGAATTCAACCTGCTCTGTCCATTATGTCAAGCAGAATAAATTTGAAGCTATTTACAAACACC
TTTACTTTTTGCACTTTTTAATTCAACATGAGTATCATATGGTATCTCTCTGGATTTCAAGGAAACACACTG
GATACTGCCTACTGACAAAACCTATTCTTCATATTTTGCTAAAAATATGTCTAAAACTTGTTTAAATATA
AATAATGTAAAAATATAATCAACTTTATTTGTCAGCATTTTGTACATAAGAAATTATTTTCAGGTTGAT
GACATCACAATTTATTTTTACTTTTGCTTTTGATTTTTAATCACAATTCCAAACTTTTGAATCC
ATAAGATTTTTTCAATGGATAAATTTCCTAAAATAAAAGTTAGATAATGGGTTTTATGGATTTCTTTGTTAT
AATATATTTTCTACCATTCCAATAGGAGATACATTGGTCAAACACTCAAACCTAGATCATTTTCTACCAA

FIG. 5

CTATGGTTGCCTCAATATAACCTTTTATTCATAGATGTTTTTTTTTATTCAACTTTTGTAGTATTTACGT
ATGCAGACTAGTCTTATTTTTTTAATTCCTGCTGCACTAAAGCTATTACAAATATAACATGGACTTTGTT
CTTTTTAGCCATGAACAAAGTGGCAAAGTTGTGCAATTACCTAACATGATATAAATTTTTGTTTTTTGCA
CAAACCAAAAGTTTAATGTTAATTCTTTTTACAAAACTATTTACTGTAGTGTATTGAAGAACTGCATGCA
GGGAATTGCTATTGCTAAAAAGAATGGTGAGCTACGTCATTATTGAGCCAAAAGAATAAATTTCATTTTT
TATTGCATTTCACTTATTGGGCTCTGGGGTTTTTTGTTTTTGTTTTTTGCTGTTGGCAGTTTAAAATATA
TATAATTAATAAAACCTGTGCTTGATCTGACATTTGTATACATAAAAGTTTACATGAATTTTACAACAAA
CTAGTGCATGATTCACCAAGCAGTACTACAGAACAAAGGCAAATTAAAAGCAGCTTTGTGAACTTTTATG
TGTGCAAAGGATCAAGTTCACATGTTCCAACTTTCAGGTTTGATAATAATAGTAGTAACCACCTACAATA
GCTTTCAATTTCAATTAACTCCCTTGGCTATAAGCATCTAAACTCATCTTCTTTCAATATAATTGATGCT
ATCTCCTAATTACTTGGTGGCTAATAAATGTTACATTCTTTGTTACTTAAATGCATTATATAAACTCCTA
TGTATACATAAGGTATTAATGATATAGTTATTGAGAATTTATATTAACTTTTTTTTCAAGAACCCTTGGA
TTTATGTGAGGTCAAAACCAAACTCTTATTCTCAGTGGAAAACTCCAGTTGTAATGCATATTTTTAAAGA
CAATTTGGATCTAAATATGTATTTCATAATTCTCCCATAATAAATTATATAAGGTGGAAAAAAAAAAAAA
AAAAAAAAAAAAAAA

SEQ ID NO:7

GenBank® GI No.:12642272; GB No:AAK00218.1; AF225986_1 voltage-gated sodium channel alpha subunit splice variant SCN3A-s [Homo sapiens]

MAQALLVPPGPESFRLFTRESLAAIEKRAAEEKAKKPKKEQDNDDENKPKPNSDLEAGKNLPFIYGDIPP
EMVSEPLEDLDPYYINKKTFIVMNKGKAIFRFSATSALYILTPLNPVRKIAIKILVHSLFSMLIMCTILT
NCVFMTLSNPPDWTKNVEYTFTGIYTFESLIKILARGFCLEDFTFLRDPWNWLDFSVIVMAYVTEFVDLG
NVSALRTFRVLRALKTISVIPGLKTIVGALIQSVKKLSDVMILTVFCLSVFALIGLQLFMGNLRNKCLQW
PPSDSAFETNTTSYFNGTMDSNGTFVNVTMSTFNWKDYIGDDSHFYVLDGQKDPLLCGNGSDAGQCPEGY
ICVKAGRNPNYGYTSFDTFSWAFLSLFRLMTQDYWENLYQLTLRAAGKTYMIFFVLVIFLGSFYLVNLIL
AVVAMAYEEQNQATLEEAEQKEAEFQQMLEQLKKQQEEAQAVAAASAASRDFSGVGGLGELLESSSEASK
LSSKGAKEWRNRRKKRRQREHLEGNNKGERDSFPKSESEDSVKRSSFLFSMDGNRLTSDKKFCSPHQSLL
SIRGSLFSPRRNSKTSIFSFRGRAKDVGSENDFADDEHSTFEDSESRRDSLFVPHRHGERRNSNGTTTET
EVRKRRLSSYQISMEMLEDSSGRQRAVSIASILTNTMEELEESRQKCPPCWYRFANVFLIWDCCDAWLKV

FIG. 5

KHLVNLIVMDPFVDLAITICIVLNTLFMAMEHYPMTEQFSSVLTVGNLVFTGIFTAEMVLKIIAMDPYYY
FQEGWNIFDGIIVSLSLMELGLSNVEGLSVLRSFRLLRVFKLAKSWPTLNMLIKIIGNSVGALGNLTLVL
AIIVFIFAVVGMQLFGKSYKECVCKINDDCTLPRWHMNDFFHSFLIVFRVLCGEWIETMWDCMEVAGQTM
CLIVFMLVMVIGNLVVLNLFLALLLSSFSSDNLAATDDDNEMNNLQIAVGRMQKGIDYVKNKMRECFQKA
FFRKPKVIEIHEGNKIDSCMSNNTGIEISKELNYLRDGNGTTSGVGTGSSVEKYVIDENDYMSFINNPSL
TVTVPIAVGESDFENLNTEEFSSESELEESKEKLNATSSSEGSTVDVVLPREGEQAETEPEEDFKPEACF
TEGCIKKFPFCQVSTEEGKGKIWWNLRKTCYSIVEHNWFETFIVFMILLSSGALAFEDIYIEQRKTIKTM
LEYADKVFTYIFILEMLLKWVAYGFQTYFTNAWCWLDFLIVDVSLVSLVANALGYSELGAIKSLRTLRAL
RPLRALSRFEGMRVVVNALVGAIPSIMNVLLVCLIFWLIFSIMGVNLFAGKFYHCVNMTTGNMFDISDVN
NLSDCQALGKQARWKNVKVNFDNVGAGYLALLQVATFKGWMDIMYAAVDSRDVKLQPVYEENLYMYLYFV
IFIIFGSFFTLNLFIGVIIDNFNQQKKKFGGQDIFMTEEQKKYYNAMKKLGSKKPQKPIPRPANKFQGMV
FDFVTRQVFDISIMILICLNMVTMMVETDDQGKYMTLVLSRINLVFIVLFTGEFVLKLVSLRHYYFTIGW
NIFDFVVVILSIVGMFLAEMIEKYSVSPTLFRVIRLARIGRILRLIKGAKGIRTLLFALMMSLPALFNIG
LLLFLVMFIYAIFGMSNFAYVKKEAGIDDMFNFETFGNSMICLFQITTSAGWDGLLAPILNSAPPDCDPD
TIHPGSSVKGDRGDPSVGIFFFVSYIIISFLVVVNMYIAVILENFSVATEESAEPLSEDDFEMFYEVWEK
FDPDATQFIEFSKLSDFAAALDPPLLIAKPNKVQLIAMDLPMVSGDRIHCLDILFAFTKRVLCESGEMDA
LRIQMEDRFMASNPSKVSYEPITTTLKRKQEEVSAAIIQRNFRCYLLKQRLKNISSNYNKEAIKGRIDLP
IKQDMIIDKLNGNSTPEKTDGSSSTTSPPSYDSVTKPDKEKFEKDKPEKESKGKEVRENQK

SEQ ID NO:8

GenBank® GI No.:6981509; Ref. No.:NM_013119.1|;Rattus norvegicus sodium channel, voltage-gated, type III, alpha polypeptide (Scn3a), mRNA

CAGTGTTTTGTCGTTTGCGCAATGGCGTGTGTCTGCCAGTAGATGGCAGTGACACGTTGAGTGCCGCCAA
CCTTTTCTTTTTTCTTTCTTTTTTTTTTTTTTTTCCCCTTCCAGGGCCGTTTTCTGATATATGTTGGGTAC
CATAGAGTGAATCTCAGAACAGGAAGCGGAGGCATAAGCAGAGAGGATTCCGGAAAGGTCTCTTTGTTTT
CATGTCCACAGAGAAAGCAAGGGGGAAAAATTGAATGTAATTTGCAAATCCCTGTGGCCCAAATCTGAAG
AACTACAGGGGGTGGCACCGTCCATTCTAACCATCTTGGATGCTGTCCTTTGTTGAGCTGTGATTCCTAA
GGCTCTCCATCAGGCAATTCTTATGCAAGAAGCTAAACGTAATTAAATGTGCAGGATGAAAAGATGGCCC
AGGCACTGCTGGTACCCCCGGGACCTGAGAGCTTCCGCCTTTTCACTCGAGAATCTCTTGCTGCTATCGA

FIG. 5

AAAGCGTGCTGCAGAAGAGAAAGCCAAGAAACCCAAGAAAGAGCAAGACATTGACGATGAGAACAAACCA
AAGCCAAACAGCGACTTGGAAGCTGGGAAGAACCTTCCATTTATCTATGGAGACATTCCTCCAGAGATGG
TGTCAGAGCCCCTGGAGGACCCTACTATGTCAGTAAGAAAACTTTTGTAGTGTTGAATAAAGG
GAAGGCGATTTTTCGATTCAGCGCCACCTCCGCCCTGTATATTTTAACTCCGCTAAACCCTGTTAGGAAA
ATTGCCATTAAGATTTTGGTACACTCTTTGTTCAGCATGCTTATCATGTGCACTATTTTGACCAACTGTG
TATTTATGACGTTGAGTAATCCTCCCGACTGGACAAAGAATGTAGAGTATACGTTCACTGGGATCTATAC
CTTTGAGTCACTTATATAAAGATCTTGGCAAGAGGTTTTGCTTAGAAGATTTCACTTTCCTCCGTGACCCA
TGGAACTGGCTGGATTTCAGTGTCATCGTGATGGCATATGTGACAGAGTTTGTGGACCTGGGCAATGTCT
CAGCGCTGAGAACGTTCAGAGTTCTCCGAGCATTGAAAACAATATCAGTCATTCCAGGTTTTAAAGACCAT
CGTGGGGGCCCTGATCCAGTCCGTGAAGAAGCTGTCCGACGTCATGATCCTCACCGTGTTCTGTCTCAGT
GTCTTTGCTCTAATCGGGCTGCAGCTCTTCATGGGCAACCTGAGGAATAAATGCTCGCAGTGGCCCCCGA
GCGATTCGGCTTTTGAAACCAACACTACTTCCTACTTCAATGGCACAATGGATTCAAATGGGACATTTGT
TAATGTAACAATGAGCACTTTCAACTGGAAGGATTATATCGCAGATGACAGTCACTTTTATGTCTTGGAT
GGACAAAAAGATCCTTTACTCTGTGGAAATGGCTCCGATGCAGGACAATGTCCAGAAGGGTACATCTGTG
TGAAGGCTGGACGAAACCCCAACTACGGCTACACAAGCTTTGACACCTTCAGCTGGGCCTTCTTGTCCCT
GTTTCGACTCATGACTCAGGACTACTGGGAGAATCTTTACCAGTTGCATTGCGTGCAGCTGGGAAAACC
TACATGATATTTTTCGTCCTGGTAATTTTCTTGGGCTCGTTTTATTTGGTGAACTTGATCCTGGCTGTGG
TGGCCATGGCCTATGAGGAGCAGAACCAGGCCACACTGGAGGAGGCTGAACAGAAGGAGGCAGAGTTTCA
GCAGATGCTGGAGCAACTGAAGAAGCAGGAGGAGGCTCAGGCAGTGGCTGCAGCCTCCGCGGCATCC
AGAGACTTCAGTGGAATAGGAGGGTTAGGAGAACTTCTTCAGAAGCTTCCAAGTTGAGCT
CCAAGAGTGCTAAGGAGTGGAGGAACCGGAGGAAGAAGGAGGAGACAGAGGAACACTTGGAGGGAAACCA
CAGAGCCGATGGAGACAGGTTTCCCAAGTCGGAATCGGAACGAAGAAGCTTCCTGCTC
TCCCTGGATGGCAACCCGCTGACTGGTGACAAGAAGCTGTGCTCTCCCCACCAGTCTCTCTTGAGTATCC
GTGGCTCCCTGTTTTCCCCAAGACGCAATAGCAAAACGAGCATTTTCAGCTTCAGAGGTCGGGCGAAGGA
CGTGGGGTCTGAGAATGACTTTGCAGACGATGAGCACAGCGAGAGCAGGAGACAC
TCCCTGTTTGTGCCGCACAGACCTGGAGAGCGACGCAACAGTAACGGTACCACCACTGAAACGGAAGTCA
GGAAGAGAAGGCTAAGTTCTTACCAGATTTCAATGGAAATGCTGGAGGATTCCTCTGGAAGACAAAGATC
CATGAGCATAGCCAGTATCCTGACCAACACCATGGAGGAACTTGAAGAATCTAGACAGAAGTGCCCACCA
TGCTGGTATAGATTCGCCAATGTGTTTTTGATCTGGGACTGCTGTGATGCATGGTTAAAAGTGAAGCATC
TTGTGAATTTAATTGTGATGGATCCATTTGTTGATCTTGCCATAACAATTTGCATCGTATTAAATACACT
GTTCATGGCCATGGAGCACTATCCCATGACCCAGCAGTTCAGCAGTGTGCTGACTGTGGGAAACCTGGTC
TTCACTGGGATCTTCACAGCCGAAATGGTCCTTAAAATCATTGCCATGGACCCCTATTATTATTTCCAAG
AGGGCTGGAATATTTTCGATGGAATTATTGTTAGCCTGAGTTTAATGGAGCTAGGCCTGGCAAATGTGGA
GGGGCTGTCTGTGCTTCGGTCCTTCAGACTGCTCCGAGTCTTCAAGTTGGCAAAGTCCTGGCCCACACTG

FIG. 5

AACATGCTCATTAAGATCATCGGCAACTCGGTGGGCGCACTGGGCAACCTGACCCTGGTGCTGGCCATCA
TCGTCTTCATTTTTGCCGTGGTCGGCATGCAGCTGTTTGGAAAGAGCTACAAGGAGTGTGTCTGCAAGAT
CAATGTGGACTGCAAGCTGCCGCGCTGGCACATGAACGACTTCTTCCACTCCTTCCTGATCGTGTTCCGA
GTGCTGTGTGGGAGTGGATAGAGACCATGTGGGACTGCATGGAGGTCGCGGGCCAGACCATGTGCCTTA
TTGTGTTCATGTTGGTCATGGTGATTGGGAACCTTGTGGTTCTGAACCTCTTTCTGGCCTTATTGTTGAG
TTCCTTTAGTTCAGATAACCTTGCTGCTACTGACGATGATAACGAAATGAACACAACCTCCAGATCGCGGTG
GGAAGGATGCAAAAGGGAATTGATTTTGTGTGAAAAATAAGATACGGGAGTGCTTCCGAAAAGCGTTTTTCA
GAAAGCCGAAAGTGATAGAAATCCAAGAAGGCAACAAAATAGACAGCTGCATGTCCAATAACACGGGCAT
CGAAATAAGCAAAGAGCTTAACTACCTTAAAGACGGTAATGGAACCACCAGCGGCGTGGGAACCGGAAGC
AGTGTGGAAAAATACGTAATCGATGAAAATGACTACATGTCATTCATTAAACAATCCCAGCCTCACCGTGA
CTGTGCCAATTGCTGTGGGAGAGTCTGACTTTGAAAATTTAAATACGGAAGAGTTCAGCAGTGAGTCAGA
ATTGGAAGAAAGTAAGGAGAAATTAAATGCAACCAGCTCTTCTGAAGGAAGCACAGTTGATGTTGCTCCA
CCCCGAGAAGGTGAACAAGCAGAAATTGAACCTGAGGAGGACCTTAAGCCAGAAGCTTGTTTTACTGAAG
GGTGCATTAAAAAATTCCCCTTCTGTCAAGTAAGTACAGAAGAAGGTAAAGGAAAAATATGGTGGAATCT
TAGGAAGACATGCTACAGCATTGTGGAGCACAACTGGTTTGAGACATTCATTGTGTTCATGATTCTCCTC
AGTAGTGGCGCTTTGGCCTTTGAGGATATATACATTGAGCAACGAAAGACGATCAAGACCATGCTGGAGT
ATGCAGACAAGGTCTTCACGTACATCTTCATCCTGGAGATGCTCCTCAAATGGGTGGCCTATGGATTTCA
AACCTATTTCACCAATGCCTGGTGCTGGTTGGACTTCCTGATCGTTGATGTTTCTTTGGTTAGCCTGGTA
GCCAATGCTCTTGGTTACTCAGAACTTGGTGCCATCAAATCCCTACGGACACTGAGAGGCTCTGAGGCCGC
TCCGAGCCTTATCCCGCTTTGAAGGCATGAGGGTGGTTGTAAATGCTCTTGTTGGTGCAATTCCCTCCAT
CATGAATGTGTTATTGGTGTGTCTCATCTTCTGGCTGATTTTTAGCATCATGGGTGTGAATCTGTTTGCT
GGAAAGTTCTATCACTGTGTTAACACGACAACAGGCAACATGTTTGAAATAAAAGAAGTGAACAATTTCA
GTGACTGTCAGGCTCTTGGCAAGCAAGCCCGGTGGAAGAATGTGAAAGTCAACTTTGACAACGTTGGGGC
TGGCTACCTGGCATTGCTGCAAGTGGCCACATTCAAAGGCTGGATGGACATCATGTATGCAGCTGTTGAT
TCGCGGGACGTCAAACTGCAGCCCATATATGAAGAAAACCTGTACATGTACTTTGTCATCTTCA
TCATCTTCGGCTCGTTCTTCACTCTAAATCTATTCATCGGTGTCATCATAGACAACTTCAACCAGCAGAA
GAAGAAGTTTGGAGGTCAAGACATCTTTATGACAGAAGAACAGAAATACTACAATGCAATGAAGAAG
CTCGGCTCAAAGAAACCTCAGAAGCCCATCCCTCGGCCTGCAAACAAATTTCAAGGGATGGTCTTTGATT
TTGTAACCAGACAAGTGTTTGACATCAGCATCATGATCCTCATCTGCCTCAACATGGTGACCATGATGGT
GGAAACGGATGACCAGAGCAAATACATGACCCTGGTTTTGTCCCGAATCAACCTAGTGTTCATTGTCCTC
TTCACTGGGGAGTTTCTGCTGAAGCTCATCTCCCTCAGATACTACTTCACGATAGGGTGGAACATCT
TTGACTTTGTGGTGGTGATTCTCTCGATTGTAGGAATGTTTCTCGCAGAGCTGATAGAGAAGTATTTCGT
GTCCCCTACCCTGTTCCGAGTCATCCGCCTGGCCAGGATTGGACGAATCCTACGCCTGATCAAAGGCGCC
AAGGGGATCCGCACTCTGCTCTTTGCTTTGATGATGTCCCTTCCTGCGCTGTTCAACATCGGCCTCCTGC

FIG. 5

TTTTCCTGGTCATGTTCATCTACGCCATCTTTGGGATGTCCAACTTTGCCTATGTTAAAAAAGAGGCTGG
AATTGATGACATGTTCAACTTTGAGACTTTTGGCAACAGCATGATCTGCTTGTTCCAAATCACCACCTCT
GCCGGCTGGGACGGACTGCTGGCCCCCATCCTCCAACAGCGCACCTCCCGATGTGACCCCGATGCAATTC
ACCCTGGAAGCTCGGTGAAGGGGGACTGTGTGGGAACCCATCCGTGGGGATTTTCTTTTTTTGTCAGCTACAT
CATCATATCCTTCCTGGTGGTGGTGAACATGTACATCGCTGTCATCCTGGAGAACTTCAGCGTCGCCACC
GAAGAAAGTGCAGAGCCCCCTGAGTGAGGACGACTTTGAGATGTTCTACGAGGTCTGGGAGAAGTTCGACC
CTGACGCCACTCAGTTCATAGAGTTCTGCAAGCTTTCTGACTTTGCAGCTGCCCTGGATCCTCCCCTCCT
CATCGCAAAGCCAAACAAAGTCCAGCTCATTGCCATGGTGAGTGGAGACCGCATCCAC
TGCCTGGACATCTTGTTTGCTTTTACAAAGCGGGTCCTGGGCGAGAGTGGAGAGATGGACGCTCTTCGAA
TCCAGATGGAAGATCGCTTCATGGCTTCCAACCCCTCCAAGGTCTCTTATGAGCCCATTACCACCACCCT
GAAACGGAAACAAGAGGAGGTGTCTGCTATCATTCAGCGTAATTATAGATGTTATCTTTTAAAGCAA
CGGTTAAAAAACATATCGAGTAAATACGACAAAGAGACAATCAAGGGAAGGATTGACTTGCCTATAAAAG
GAGATATGGTTATTGACAAATTGAATGGGAATTCCACCCCAGAAAAGACGGATGGGAGTTCCTCCACAAC
CTCTCCTCCTTCCTATGACAGTGTAACAAAACCAGATAAGGAAAAGTTTGAGAAAGACAAACCAGAAAAA
GAAATCAAAGGGAAAGAGGTCAGAGAGAATCAAAAGTAAAAAGAGACAAAGAAATGTCTTTGTAATCAAT
TGTTTACAGCCTCTGAAGGTAAAGTATCCGTGTCAACTGGACTCTAAGGAGAGGTCCATGCCAAACTGAC
TGTTTCAACAAATACTCAAGGTCAGTGCCTATACCAGACAGTGACCTCTGTCACTGCCACTCTGTGAGAC
AGGGTATCAACATTGACAAGAGGTTGCTGCTTCCATTACCAGCTGACACTGCTGAGGAGAACTCCATTGT
GCAAGTGACCCGTCATCATGCCCCCAAACTCCATTAGTACAACGCTCCTGTCATCTATTTTTTAACATTCA
CATTTGCCATATTTTTTACAAAATCTGTCCCAGTGTATCTTCCTGGTCCCCACTTCATAGTCTGTTCATAA
TACTATGTCACTATTTTTGTAAATGAAGTTTACGTTAAGGGAAAATATATATATAAGAATCCCATGTTGC
TAAGTCCACACAAGTTTCTCCAGTAATCATAAAAAAAATATTTTGCCTGAGAGATGAAATTATTGCTCAAAAC
AAAAAAAAATAAATTCTAATGTTAACAGTTTC

FIG. 5

SEQ ID NO:9

GenBank® GI No.:6981510; Ref. No.:NP_037251.1; sodium channel, voltage-gated, type III, alpha polypeptide [Rattus norvegicus]

MAQALLVPPGPESFRLFTRESLAAIEKRAAEEKAKKPKKEQDIDDENKPKPNSDLEAGKNLPFIYGDIPP
EMVSEPLEDLDPYYVSKKTFVVLNKGKAIFRFSATSALYILTPLNPVRKIAIKILVHSLFSMLIMCTILT
NCVFMTLSNPPDWTKNVEYTFTGIYTFESLIKILARGFCLEDFTFLRDPWNWLDFSVIVMAYVTEFVDLG
NVSALRTFRVLRALKTISVIPGLKTIVGALIQSVKKLSDVMILTVFCLSVFALIGLQLFMGNLRNKCSQW
PPSDSAFETNTTSYFNGTMDSNGTFVNVTMSTFNWKDYIADDSHFYVLDGQKDPLLCGNGSDAGQCPEGY
ICVKAGRNPNYGYTSFDTFSWAFLSLFRLMTQDYWENLYQLTLRAAGKTYMIFFVLVIFLGSFYLVNLIL
AVVAMAYEEQNQATLEEAEQKEAEFQQMLEQLKKQQEEAQAVAAASAASRDFSGIGGLGELLESSSEASK
LSSKSAKEWRNRRKKRRQREHLEGNHRADGDRFPKSESEDSVKRRSFLLSLDGNPLTGDKKLCSPHQSLL
SIRGSLFSPRRNSKTSIFSFRGRAKDVGSENDFADDEHSTFEDSESRRDSLFVPHRPGERRNSNGTTTET
EVRKRRLSSYQISMEMLEDSSGRQRSMSIASILTNTMEELEESRQKCPPCWYRFANVFLIWDCCDAWLKV
KHLVNLIVMDPFVDLAITICIVLNTLFMAMEHYPMTQQFSSVLTVGNLVFTGIFTAEMVLKIIAMDPYYY
FQEGWNIFDGIIVSLSLMELGLANVEGLSVLRSFRLLRVFKLAKSWPTLNMLIKIIGNSVGALGNLTLVL
AIIVFIFAVVGMQLFGKSYKECVCKINVDCKLPRWHMNDFFHSFLIVFRVLCGEWIETMWDCMEVAGQTM
CLIVFMLVMVIGNLVVLNLFLALLLSSFSSDNLAATDDDNEMNNLQIAVGRMQKGIDFVKNKIRECFRKA
FFRKPKVIEIQEGNKIDSCMSNNTGIEISKELNYLKDGNGTTSGVGTGSSVEKYVIDENDYMSFINNPSL
TVTVPIAVGESDFENLNTEEFSSESELEESKEKLNATSSSEGSTVDVAPPREGEQAEIEPEEDLKPEACF
TEGCIKKFPFCQVSTEEGKGKIWWNLRKTCYSIVEHNWFETFIVFMILLSSGALAFEDIYIEQRKTIKTM
LEYADKVFTYIFILEMLLKWVAYGFQTYFTNAWCWLDFLIVDVSLVSLVANALGYSELGAIKSLRTLRAL
RPLRALSRFEGMRVVVNALVGAIPSIMNVLLVCLIFWLIFSIMGVNLFAGKFYHCVNTTTGNMFEIKEVN
NFSDCQALGKQARWKNVKVNFDNVGAGYLALLQVATFKGWMDIMYAAVDSRDVKLQPIYEENLYMYLYFV
IFIIFGSFFTLNLFIGVIIDNFNQQKKKFGGQDIFMTEEQKKYYNAMKKLGSKKPQKPIPRPANKFQGMV
FDFVTRQVFDISIMILICLNMVTMMVETDDQSKYMTLVLSRINLVFIVLFTGEFLLKLISLRYYYFTIGW
NIFDFVVVILSIVGMFLAELIEKYFVSPTLFRVIRLARIGRILRLIKGAKGIRTLLFALMMSLPALFNIG
LLLFLVMFIYAIFGMSNFAYVKKEAGIDDMFNFETFGNSMICLFQITTSAGWDGLLAPILNSAPPDCDPD
AIHPGSSVKGDCGNPSVGIFFFVSYIIISFLVVVNMYIAVILENFSVATEESAEPLSEDDFEMFYEVWEK
FDPDATQFIEFCKLSDFAAALDPPLLIAKPNKVQLIAMDLPMVSGDRIHCLDILFAFTKRVLGESGEMDA
LRIQMEDRFMASNPSKVSYEPITTTLKRKQEEVSAAIIQRNYRCYLLKQRLKNISSKYDKETIKGRIDLP
IKGDMVIDKLNGNSTPEKTDGSSSTTSPPSYDSVTKPDKEKFEKDKPEKEIKGKEVRENQK

FIG. 5

SEQ ID NO:10]
GenBank® GI No.:9055329; Ref. No.:NM_018732.1; Mus musculus sodium channel, voltage-gated, type III, alpha polypeptide (Scn3a), mRNA

TTTTTATATCTGTGAGGTGACGAAAGAAAAAGAAAAAGAAAAAGAAGAAATGCAAATAAAAAATGTTGAG
CCCCAGTTAATGTCAGGATTTTAATCAATTCAATTCTTATTGGAGGAACTACTTTAAAGCATGTAGAAGC
TGAGGATAGTGGTCATATCTCTAACACCAGTACTTGGGAGGTGAAGCCAGAAGAACTAGCCTAGATTTAC
TCTCAGATATATTGTAAGTTTGAGGCTAGCCTGGGCTACATGAAACTGTATCTCATCCAACACATAAAAA
AAGTTTGATATATTTGGTATATTAAACAATGATATAACAAAATGTTTAGAATTATAGCAAAAATAATTGG
TAAAAGTACCTACTATATATATATATATATACATATATACATATATATGTATACATATATACATATAT
GTATTTTTTAAATTTAACATAAGCTTTTAAAAATCGAATTATCTTACCTTTTAAAGAGAAATGTAATTCA
TATTTCAACATTCCTTTCAGTTTCTAGAGTAGAATCTGAAGTGACAGTTGATGCATTAGTAGTGTCTGTT
GTGTGCATCTGTCTGTCATTCCATCCACGCTTTGCCCACCTGTAATTAGAGACCCTTTCACACAGGCAAG
GGGCCCAGAGGTCTGCGGCAGTCTGTAATTAAAGTATTAATTTTTCTTAGGTCGATCTAAAATGAAAATA
AGTAAATCTAAAATTAGATTTATAAAGAAAAAAATGTGCTGAAATAACGACTTGATTTACAACCCTAATA
TTATTATCACCTTTTTGTTTGGAATCTACATTATGATCAACTCATAAAATAATAGTCTAGCTTCCAAGTG
TACTACATTTCCTTTTATTTCATTACAGCTGCGAGTCTTCAAGTTGGCAAAATCCTGGCCCACACTGAAT
ATGCTCATTAAGATCATCGGCAACTCGGTGGGCGCACTGGGCAACCTGACCCTGGTGCTGGCCATCATCG
TCTTCATTTTTGCCGTGGTCGGCATGCAGCTGTTTGGAAAGAGCTACAAGGAGTGTGTTTGCAAGATCAA
CGAGGACTGCAAGCTCCCGCGCTGGCACATGAACGACTTCTTCCACTCCTTCCTGATAGTGTTCCGCGTG
CTGTGTGGGGAGTGGATAGAGACCATGTGGGACTGCATGGAGGTCGCGGGCCAGACCATGTGCCTTATTG
TGTTTATGTTGGTCATGGTGATTGGGAACCTTGTGGTTCTGAACCTTTTCCTGGCCTTATTGTTGAGTTC
CTTTAGCTCAGACAACCTTGCTGCTACGGACGATGATAACGAAATGAACAACCTCCAGATCGCGGTGGGA
AGGATGCAAAAGGGGATTGATTATGTGAAAAATAAGATACGGGAGTGCTTCCGAAAAGCCTTTTTTTAGAA
AGCCGAAAGTGATAGAAATCCACGAAGGGAACAAAATAGACAGCTGCATGTCCAATAACACGGGCGTAGT
TGAAATAAGCAAAGAGCTTAACTACCTTAAAGACGGTAACGGAACCACCAGTGGCGTGGGTACTGGAAGC
AGTGTGGAGAAATACGTAATTGATGAAAATGACTACATGTCATTCATCAACAACCCCAGCCTCACCGTGA
CGGTGCCAATTGCCGTGGGAGAGTCTGACTTTGAAAATTTAAACACGGAAGAGTTTAGCAGTGAGTCAGA
ACTGGAAGAAAGCAAGGAGGTAAGCGCGCTTTTCAGTTCAGGCCACCACTTTTGCGCAATCTACACAGTA
TGGCTCCTCTGTATTGTTTTTTGCCTGTGAAGGTGCTTAATCAACAGAAAGAAATGGGTTGGGTGTGTAG
CTCAAGGGATAGGATACTTAGCATGCATGACGTCCTTGTAGTACCCAACACCACACCCAAAAGCAACTTA
AACGTAGATAAAGTTGGAACATCATGAGAAATGGGTAAGTTCGTTTAAATATAACTTTCCCATAGGAAAT

FIG. 5

CACAACTTGAGCGATTAACATGTTCATTTTCTTGATAACTGAAAGCCTGATTTAATATGCAATCCTAAAC
AAAAGAGATACTATTTAACACATTTTTCCCTCGCTAGTTATTTGTTTTAGAAAACTCAATGAACTATATT
TTAATGGTGGTATGCCATCACTGTGAAAAATTTACATAGTCTTTATTCACATTTAAGTGTTTTATTTACC
ATTTTGTTTACTAGGAAGGGTCAAGCCATACTGATATTTTTCCTATTAAAGATGAGCAAACCTATGACAT
TTTCTACATTACCTTAAAAATACTGAAGATTAACATTTGATGATTATAGTGGATCTACAGATGGGAAAAT
TTCCGTCATATGAGTAGTTGATCGAATGAAAAGAGAAAATTTTCATATGCTATGATTTGAGCTCATTTGG
GTCTAATGACAATAGCTTAGTGACATTACCTTCAATATTTTATTATTATTTATTTATGGCCTTTGGATGT
AACAGCTGGAGGTTAATCTAGCACAGATGGTGTTATAAAGGATCTCTAGCTGGAGGGAATCCTCAACACC
CTGGAACAGACCAATGATGTTTGATTCTATGGATTCTCTTGGAGCTTTTGAAAACCAGTTACACCAAGAT
AATTTGCTCTAGAAATCCTTATTAGAAGTTTATGGCATCACAACTCACAGTGGTCCCATTCTTTTCATAT
TTTAGAATATGTTTTAAAACTAAAAAACATATGAACAAAATGAGGTAGCAATGTTTATTTTCACAGTTGC
ACACTAATTGTGCATAGCACATCTAATTCACGTTGCTCATCCTAGTAGCTAAGACTCAATTCTGGCTTTA
TTTTCTATCACCTGGCGTAGAATTGACTTACAAAGGAACCCTAGAGGACTAGCAGGCATTCACTGACTAT
TTTGTCCAATTCGGTCAAAGACAGTCTTTATCAAGTGGTTCCCAACAAACTCATAAAGTCATTAAAACTC
TATTTAATTGATCTTACAGGCCGGTGTTAAATTCTTAGGCGTTTAAGAATGGGAAGGGAGGTTAAATGAC
AGAAAATTGTAATAGGCCTCATATTTGGGTCACATCGTTAAAAAGTGGAAAGATACTGTTCTCCAAAGGA
GAGCCAGGGTTGATAATGAGCTCCTGTTACTCAGGCGAGTGGAGAGCAGGAGACAGGGCAAAGGATGTGC
CGGTGTGTCTGGAAGCTCCAGACTGCAGCCTTGCAGAGTAACTCGGAGCTTGGAATTGTCTGCATGGTCA
CGAAGGAGTGCTCTAAAACAGAAGCAATTAGAAAGGGGTATCCTAGGAACATCTGTTATTAAAGAGTAAA
GGACGTTAGACTGAGAGATAATGGAGATTAACTTACACACTGTTATAGCAATGAGATGGTGAAATTCTGG
GCCAAAATAATAGAGAACCAAGCGTAATTGGCAATTTAACAGACCTCAAGAATCTGAGGAATCAGAAAGT
GGCAATTCCACTGTCTGATAAGGGCTTCTGAGGAAGGTCACCAGGTTTGTATGGAAAGGAATTC

SEQ ID NO:11

GenBank® GI No.:9055330; Ref: NP_061202.1; sodium channel, voltage-gated, type III, alpha polypeptide [Mus musculus]

MLIKIIGNSVGALGNLTLVLAIIVFIFAVVGMQLFGKSYKECVCKINEDCKLPRWHMNDFFHSFLIVFRV
LCGEWIETMWDCMEVAGQTMCLIVFMLVMVIGNLVVLNLFLALLLSSFSSDNLAATDDDNEMNNLQIAVG
RMQKGIDYVKNKIRECFRKAFFRKPKVIEIHEGNKIDSCMSNNTGVVEISKELNYLKDGNGTTSGVGTGS
SVEKYVIDENDYMSFINNPSLTVTVPIAVGESDFENLNTEEFSSESELEESKEVSALFSSGHHFCAIYTV
WLLCIVFCL